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March 29, 2006, 01:38:52 ; Search time 124.25 Seconds (without alignments) 49.507 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                            2443163 seqs, 439378781 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abo73099 Pseudomon	Abo83630 Pseudomon	Adx97192 Plant ful	σ			4	Abp76678 Streptomy	Aab71432 Peptide A	0	0 Heparin	Aab71428 Peptide B	Abp00279 Human ORF	'n	8	7 Propic			8		Abo83790 Pseudomon	Abo68429 Pseudomon	Aau86821 Novel hum	Adb60155 Connectiv
SUMMARIES	ID	ABO73099	AB083630	ADX97192	AB074539	ADH48840	ADG48250	AAU33234	ABP76678	AAB71432	AAB71430	AAY87840	AAB71428	ABP00279	ADX75905	AAU41918	ABM38437	ABP00666	AAU62059	ABM58578	ABP05425	AB083790	AB068429	AAU86821	ADB60155
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7 ABO72505 8 ADX87688 7 ABO78160	7 ABO75935 8 ADX78723 7 ABO74930 7 ABO82700	4 AAU4224 6 ABM38743 6 ABO76573	ABO73028 7 ABO68892 7 ABO72617 4 AAU47602	6 ABM44121 7 ABO68472 7 ABO83595 4 AAG90194 8 ADY11827
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ALIGNMENTS

The invention relates to pseudomonas aeruginosa polypeptides and the polynuclectides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection. Bacterial infection; Pseudomonas aeruginosa infection; antibacterial. Bush D; Disclosure; SEQ ID NO 21845; 455pp; English. Rubenfield MJ, Nolling J, Deloughery C, Pseudomonas aeruginosa polypeptide #5274. ABO73099 standard; protein; 133 AA. (GENO-) GENOME THERAPEUTICS CORP. 98US-0074788P. 98US-0094190P. 99US-00252991. (first entry) Pseudomonas aeruginosa. WPI; 2003-615309/58. N-PSDB; ABD06670. 18-FEB-1999; 18-FEB-1998; 27-JUL-1998; US6551795-B1 29-JUL-2004 22-APR-2003 ABO73099;

Pred. No. 2e+03;

Similarity

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                                                                                                                                                                                ö
of Pseudomonas species using biochip technology. Sequences AB067826-AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment opathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                              Gaps
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                                                                                                                                         Score 19; DB 7; Length 133; Pred. No. 1.5e+03; 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 32376; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polypeptide #15805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                            ABO83630 standard; protein; 189 AA.
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33.3%;
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N-PSDB; ABD17201.
                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                           Sequence 133 AA;
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                                                                                                                                                                                                                                                                                                           RESULT 2
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95.0%; Score 19; DB 7; Length 189;

Query Match

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence in the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, heatbicides, extreme improving plant tolerance to cold, heat, drought, herbicides, extreme improving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the call cycle pathway, for conferring increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one carbohydrate, mitrogen or phosphorus use and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
   Gaps
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   Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                      ADX97192 standard; protein; 323 AA.
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05-NOV-2001; 2001US-00985678.
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4; Conservative
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
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                                                                                                                                                                                                                                       RESULT 3
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307 RRAASRSSRTAR 318

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ADH48840 standard; protein; 533 AA
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Pred. No. 3.9e+03;
0; Mismatches 8; Indels
                                                                                                                   Score 19; DB 8; Length 323; Pred. No. 3e+03; 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa polypeptide #6714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO74539 standard; protein; 442 AA.
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Best Local Similarity 33.3%;
Matches 4; Conservative
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Lines 4; Conservative
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                                                           Sequence 323 AA;
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invention.
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Peyman JA;
, Stone DJ;
                                                                                                                                                                                          Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic; hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV53; protein-kinase-like protein; chromosome 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE; Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA; Gorman L, Guo X, Gusev VY, Kekuda R, Li L, Liu X, Malyankar UM; Miller CE, Millet I, Padigaru M, Patturajan M, Pena CEA, Peyman C Rastelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;
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                                                                                                                                             NOV53 protein sequence, SEQ ID 124.
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2001US-0272404P.
2001US-0272410P.
2001US-0272414P.
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2001US-0285754P.
2001US-0286096P.
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2001US-0311981P.
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                                                                                                 25-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-698672/75.
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                                                                                                                                                                                                                                                                                                                                                     WO200268652-A2.
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02-MAR-2001;
02-MAR-2001;
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16-MAR-2001;
20-MAR-2001;
20-MAR-2001;
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30-MAR-2001;
02-APR-2001;
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Miller CE, M
Rastelli L,
Taupier RJ,
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2001;
23-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001;
31-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2001;
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95.0%; 33.3%;

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Gaps

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Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                          Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 738-739; 765pp; English
                                                            AAU33234 standard; protein; 644 AA.
                                                                                                                                     Novel human secreted protein #3725.
                                                                                                                                                                                                                                                                                      16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                                             18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT;
                                                                                                             (first entry)
56 RRARAATSRAAR 67
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                           rang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 644 AA;
                                                                                                                                                                                                                                      WO200179449-A2.
                                                                                                                                                                                                               Homo sapiens.
                                                                                                             18-DEC-2001
                                                                                                                                                                                                                                                              25-OCT-2001
                                                                                    AAU33234;
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Matches
                                              AAU33234
ID AAU
                                     RESULT
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                                The present invention relates to novel human NOVX proteins, where X is any number from 1 to 91 and their coding sequences. The proteins and coding sequences are useful for preventing or treating disorders or syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV53 is a protein kinase-like protein and its coding sequence maps to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding retinal protein sNETO1, useful for diagnosis of retinal disease, especially macular degeneration, also for drug screening
                                                                                                                                                                                                                                                                                                                                                                                      human; retina-specific protein; NETO1; retinal disease;
age related macular degeneration; night blindness; protein kinase A203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retina-specific protein - NETO1. The DNA and protein sequences of the invention are useful in the treatment of retinal diseases, auch as macular degeneration (especially age related) and night blindness. The present amino acid sequence represents human retina-specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequences of a human
                                                                                                                                                                           Gaps
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0
                                                                                                                                                 Score 19; DB 5; Length 533;
Pred. No. 4.5e+03;
0; Mismatches 8; Indels
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33.3%; Pred. No. 4.5e+03;
ive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                               Human retina-specific protein kinase A203.
                                                                                                                                                                                                                                                                                        ADG48250 standard; protein; 534 AA.
            Claim 1; Page 298; 923pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goehring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Fig 6; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LYNK-) LYNKEUS BIO TECH GMBH
                                                                                                                                                  95.0%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002; 2002EP-00003675.
21-FEB-2002; 2002US-0357857P.
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                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                         4; Conservative
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                                                                                                                                                                                                                          56 RRARAATSRAAR
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N-PSDB; ADG48249.
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                                                                                                                          Sequence 533 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                              RESULT 6
ADG48250
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polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent of or use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins to express them are also useful for producing the proteins. The proteins as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or etimulation, as anti-inflammatory agents; and in treatment of leukaemias. AMU25510-AMU3304 represent the amino acid sequences of novel human corrected proteins of the invention
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The invention relates to novel human secreted polypeptides.
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Pred. No. 5.2e+03;
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33.3%;
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Conservative

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immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra - Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for the treatment of sepsis and the detection and removal of endotoxins. The peptides of the invention are used in a method for detecting endotoxin in a sample comprising contecting the sample with a labelled helix peptide and then detecting the semence of any labelled molecule bound to and then detecting the presence of any labelled molecule bound to and then detecting the presence of any labelled molecule bound to anotoxin. The peptides expansions the sample which comprises exposing the sample to a helix peptide, bound to a solid support, then collecting the sample. The anotoxin removal may be in vivo, or the peptides may be used to form an affinity trap for endotoxins in e.g. dialysis-type treatments, or for removal of endotoxins from plasma fractionation products. They are also used as model frameworks for endotoxin binding from which new analogues may be designed. This sequence represents the peptide Arg Helix #3 which is used in the construction of the branched chain peptide Tris-Arg Helix. #3 described in the method of the invention
                                                                                                                                                                                                                                                                                              Use of cationic helix peptides for treatment of sepsis and for the detection and removal of endotoxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sepsis; branched chain peptide; antibacterial; immunosuppressive; endotoxin; helix peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Ala is modified by unidentified R1 group"
                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel use of antibacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 5; I
Pred. No. 4.9e+02;
0; Mismatches 8;
                                                                                                                                                                    (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide Tris-Arg Helix #3 fragment.
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                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 2, 18pp; English
                                                                                                                                                                                                                Wolz G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2002; 2002EP-00251027
                                                                                                                              14-FEB-2001; 2001US-0268410P
                                                                                  14-FEB-2002; 2002EP-00251027
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ilarity 33.3%;
Conservative
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                                                                                                                                                                                                                Wolz RL,
                                                                                                                                                                                                                                                        WPI; 2002-659478/71
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Best Local Similarity
Matches 4; Conserv
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Modified-site
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EP1232754-A2
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                                            21-AUG-2002
                                                                                                                                                                                                                Harris RB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
                                                                                                          Avilamycin, antibacterial, virucide, protozoacide, fungicide, infection, medicine, Staphylococcus aureus, biosynthetic gene cluster, enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "This residue has a side chain C(O)-NepsilonH-(CH2)3-Tris-ArgHel#3 , where the Tris-ArgHel#3 is represented in AAB71431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                  Streptomyces viridochromogenes Avi gene cluster polypeptide frame 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New avilamycin derivatives, useful for treatment of infections, and nucleic acid encoding avilamycin synthesis enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sepsis; branched chain peptide; antibacterial; immunosuppressive; endotoxin; helix peptide.
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Pred. No. 7.6e+04;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide Arg Helix #3 for construction of Tris-Arg helix #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bechthold A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Acylated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Trefzer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 68-301; 319pp; German
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                                                                                                                                                                                                                                                                                                                                                                                           (COMB-) COMBINATURE BIOPHARM AG
                                                                                                                                                                           Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                         24-AUG-2001; 2001WO-EP009815.
                                                                                                                                                                                                                                                                                                                                                   25-FEB-2001; 2001DE-01009166.
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Similarity 33.3%;
4; Conservative
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                            (first entry)
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                       WO200268436-A1
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Modified-site
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                            26-FEB-2003
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ABZ37516)

Synthetic.

AAB71432;

AAB7143;

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Length 15; 8; Indels

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mammal by reducing the anticoagulant effects of heparin.
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-659478/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                     immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra
-Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
-Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
the treatment of sepsis and the detection and removal of endotoxins. The
peptides of the invention are used in a method for detecting endotoxin in
a sample comprising contacting the sample with a labelled helix peptide
and then detecting the presence of any labelled molecule bound to
endotoxin. The peptides can also be used in a method for removing
endotoxin in a sample which comprises exposing the sample to a helix
peptide, bound to a solid support, then collecting the sample. The
endotoxin removal may be in vivo, or the peptides may be used to form an
affinity trap for endotoxins in e-g dialysis-type treatments, or for
removal of endotoxins from plasma fractionation products. They are also
used as model frameworks for endotoxin binding from which new analogues
may be designed. This sequence represents the peptide Arg Helix #3 which
is used in the construction of Tris-Arg Helix #3, a branched chain
peptide described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                  Use of cationic helix peptides for treatment of sepsis and for the detection and removal of endotoxins.
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                                                                                                                                                                                                                                                                                                           This invention describes a novel use of antibacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 5; Length 16;
Pred. No. 5.2e+02;
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                                                  (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparin binding peptide Bis-Arg helix #2.
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protamine substitute; treatment.
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    14-FEB-2001; 2001US-0268410P
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RRAARAAARAK 13
                                                                                                Wolz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sobel M;
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                                                                                                                                         WPI; 2002-659478/71
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                                                                                                Harris RB,
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RESULT 11

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This invention describes novel heparin binding molecules (I). The molecules (I) are useful as heparin antagonist drugs for cardiovascular application and specifically neutralize heparin's conventional anticoagulant properties. (I) are also useful for counteracting actions of heparin locally e.g. in bleeding wounds, vascular ansatomoses or leaking prosthetic vascular grafts. (I) is also useful combined in a pharmaceutical composition with insulin, as a substitute for protamine for use in treating diabetics. The heparin binding molecules (I) specifically neutralize heparin's conventional anticoagulant properties without causing deleterious hemodynamic side-effects or exacerbation of the proliferative vascular response to injury. (I) are short duration, intravenous drugs to be used in elective or emergency situations which can safely and specifically neutralize heparin's proliferative response to injury. This sequence represents a heparin's proliferative response to injury. This sequence represents a heparin's proliferative response to injury. This sequence represents a heparin's proliferative response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of cationic helix peptides for treatment of sepsis and for the detection and removal of endotoxins.
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Pred. No. 5.9e+02;
0; Mismatches 8; Indels
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Example 1; Fig 1a; 39pp; English
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peptides of the invention are used in a method for detecting endotoxin in a sample comprising contacting the sample with a labelled helix peptide and then detecting the presence of any labelled molecule bound to endotoxin. The peptides can also be used in a method for removing endotoxin in a sample which comprises exposing the sample to a helix peptide, bound to a solid support, then collecting the sample. The endotoxin removal may be in vivo, or the peptides may be used to form an affinity trap for endotoxins in e.g. dialysis-type treatments, or for removal of endotoxins from plasma fractionation products. They are also used as model frameworks for endotoxin binding from manalogues may be designed. This sequence represents the peptide Arg Helix #2 which is used in the construction of Bis-Arg Helix #2, a branched chain peptide described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
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Pred. No. 5.9e+02;
0; Mismatches 8; Indels
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29-AUG-2000; 2000US-0228716P.
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33.3%;
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 AA;
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disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide squareness can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, pooriasis, benign tumours, keloid, degenerative disorders, haemorrhage, catecoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases mellitus, systemic currents of the sases, various immune deficiencies and disorders, infectious attenties, autoimmune disorders such as multiple sclerosis, rheumatoid catebases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also the degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, repertusion injury in various tissues and conditions resulting from repertusion injury in various tissues and conditions resulting from the parinted spacification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from NIPO at fip.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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Pred. No. 1.4e+03;
0; Mismatches 8; Indels
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05-NOV-2001; 2001US-00985678.
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33.3%;
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Best Local Similarity
4; Conserve
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ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                             Sequence 59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADX75905;
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(CAOY/)
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treating acne vulgaris.

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at trp. seqdata.uspto.gov/sequence.html?DocID:2004034088. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, heatbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert in polynerics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 18; DB 8; Length 64; 33.3%; Pred. No. 1.5e+03; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #2814.
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                                                                     Claim 1; SEQ ID NO 45271; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU41918 standard; protein; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001; 2001WO-US012865.
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s J, Zhang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                    pests, for confeimproving yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001.
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Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for

WPI; 2001-616774/71. N-PSDB; AAS59515.

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaria. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies opperation of acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes polypeptides and crivity of P. acnes polypeptides and carryme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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Pred. No. 1.8e+03;
0; Mismatches 8; Indels
                                                    Example 1; SEQ ID NO 3113; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 29, 2006, 01:44:11 Job time : 127.25 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.0%;
Best Local Similarity 33.3%;
Matches 4; Conservative (
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 29, 2006, 01:44:43; Search time 20.5625 Seconds (without alignments) 65.509 Million cell updates/sec Run on:

US-10-712-447-210 20 Perfect score:

Title:

1 XXRRXXXXXXXX 14 **BLOSUM62** Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	nuclear basic prot	н		hetical pr	cyaE protein - Bor	transpo	hypothetical prote			hypothetical prote	hypothetical prote	splicing factor, a	hypothetical prote	probable transposa	hypothetical prote	spliling factor SR	hypothetical prote	hypothetical prote	probable proteinas	conserved hypothet	probable PHD-type	hypothetical prote	probable calcium c	probable potassium	hypothetical prote	DNA (cytosine-5-)-	hypothetical prote	ਲ	sperm chromatin pr
ar er	865036	JH0404	T30752	T18918	BVBRCE	T14162	D72453	AI3144	B98143	G72697	D87267	A57198	G70705	T29423	PQ0339	S59043	E82796	T36706	A70837	E87435	T40911	T15340	B85045	T31354	T19722	JE0378	G71415	A46068	PN0081
DB	N	N	~	~	н	~	7	7	7	7	7	~	7	~	N	N	~	N	7	7	7	~	7	~	7	7	7	7	~
Length	79	79	110	197	474	574	99	668	710	1.95	207	238	241	310	317	344	395	436	461	520	571	717	724	1017	1577	1622	2351	3144	25
Query	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	80.0
Score	1	18	18	18	18	18	18	18	18	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	16
Result No.	-	8	m	4	S	v	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote protamine Pl - duc nucleocapaid prote ribosomal protein 30s ribosomal prot late embryogenesis ribosomal protein sperm protein gent protein hypothetical prote	hypothetical prote protein limported hypothetical prote hypothetical prote pli2 hypothetical hypothetical
E86930 \$39425 VANVBM AA2815 AC2616 B97398 \$239941 G87249 \$31225	D71162 C95386 B72683 T14796 A26882 G75510
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57 61 65 79 88 88 88 90 91	1126 1126 1144 1184 1184
0000000000	000000
	10 10 10 10 10
0 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	v 4 4 4 4 4 4 v O H G W 4 R

ALIGNMENTS

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Cispecies: Xenopus laevis (African clawed frog)
Cipate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
Cipate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
Rightyoshi, H.; Uno, S.; Yokota, T.; Katagiri, C.; Nishida, H.; Takai, M.; Agata, K.; Egu Exp. Cell Res. 194, 95-99, 1991
Exp. Cell Res. 194, 95-99, 1991
A;Fitle: Isolation of cDNA for a Xenopus sperm-specific basic nuclear protein (SP4) and A;Reference number: JH0404; MUID:91200205; PMID:2015853 RESULT 2

A;Molecule type: mRNA A;Residues: 1-79 AHIY>
A;Residues: 1-79 AHIX>
A;Cross-references: UNIPROT:P24056; UNIPARC:UPI0000000606; GB:D00916; NID:g222970; PIDN
A;Experimental source: round spermatid
A;Accession: PU0021

A;MOJECUJE type: protein
A;Residues: 2-11;12-43;65-74;75-79 <HIZ>
A;Cross-references: UNIPARC:UP1000017BF78; UNIPARC:UP1000017BF79; UNIPARC:UP1000017BF7A,
A;Cross-references: UNIPARC:UP1000017BF78; UNIPARC:UP1000017BF7A,
B;Mita, K.; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagiri, C.
Biochim. Biophys Acta 1455, 430-438, 1995
A;Title: Structure of genes for sperm specific nuclear basic protein (SP4) in Xenopus 1-A;Reference number: S65036; MUID:96125743; PMID:8541323

Wed Mar 29 18:01:20 2006

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hypothetical protein C04G2.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18918
                                                                                              R;Hembry, C. submitted to the EMBL Data Library, April 1996 A;Reference number: Z19045 A;Accession: T18918 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 2;
Pred. No. 1e+02;
0; Mismatches 8
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: cyclolysin transport; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyaE protein - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                     90.0%;
33.3%;
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Best Local Similarity 33.3%;
Matches 4; Conservative
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C;Superfamily: cyaE protein
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A, Gene: CESP: C04G2.8
                                                                                                                                                                                                                                                                                                                                                        position: 4
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BVBRCE
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                          A; Molecule type: DNA
A; Residues: 1-79 < ANIT.
A; Residues: 1-79 < ANIT.
A; Residues: 1-79 < ANIT.
A; Cross-references: UNIPARC:UPI00000006D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PI
A; Experimental source: strain J
A; Genetics: CH1
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-79 < MIS
A; Experimental source: strain J
A; Experimental source: strain J
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T30752

Mypotherical protein 150R - Molluscum contagiosum virus 1

NyAlternate names: MC150R

C;Species: Molluscum contagiosum virus 1

C;Species: Molluscum contagiosum virus 1

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T30752

R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.

Science 273, 813-816, 1996

A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: 220876; MU19:96335459; PMID:8670425

A;Accession: T30752
                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Kesdides: 1-79 AMIW>
A,Cross-treferences: UNIPARC:UPI00000D6D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PI
A,Experimental source: strain J
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C;Superfamily: Molluscum contagiosum virus 1 hypothetical protein 150R
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A; Note: the authors translated the codon TAT for residue 73 as Thr
A; Accession: S65039
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Genetics: CH3
A;Note: the authors translated the codon TAT for residue 73 as Thr
C;Genetics: <CH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 18; DB 2; Length 110; 33.3%; Pred. No. 61; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;2-79/Product: basic nuclear protein SP4 #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
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Pred. No. 46;
0; Mismatches
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33.3%;
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Best Local Similarity
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Best Local Similarity
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A;Residues: 1-110 <SI
         A; Accession: S65037
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C;Genetics: <CH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 76/1
C;Genetics: <CH3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: XLSP42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: XLSP43
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RESULT T18918

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A;Molecule type: DNA
A;Residues: 1-474 <GLA>
A;Residues: 1-474 <GLA>
A;Cross-references: UNIPROT:P11092; UNIPARC:UPI000012889E; EMBL:X14199; NID:g39731; PIDN:
C;Comment: This protein is required for the transport of cyclolygin (or calmodulin-sensit lease into the external medium. This secretion process is very similar to that of the E.
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C;Species: Mycobacterium smegmatis
C;Species: Mycobacterium smegmatis
C;Date: 20.Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14162
R;Yu, S.; Fiss, E.; Jacobs Jr., W.R.
R;Yu, S.; Fiss, E.; Jacobs Jr., W.R.
A;Title: Analysis of the exochelin locus in mycobacterium smegmatis: biosynthesis genes }
A;Reference number: 217898; MUID:98389687; PMID:9721311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT:087312; UNIPARC:UPI00000B60F3; EMBL:AF027770; NID:g3560502; I
C; Superfamily: Streptomyces glaucescen ABC transporter strV; ATP-binding cassette homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ridlaser, P.; Sakamoto, H.; Bellalou, J.; Ullmann, A.; Danchin, A. EMBO J. 7, 3997-4004, 1988
A.itle: Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase--haemolysin A.Reference number: S02386; MUID:89091151; PMID:2905265
A.Rocession: S02388
A;Reduces: 1-197 <WIL>
A;Reduces: 1-197 <WIL>
A;Cross-references: UNIPROT:Q17626; UNIPARC:UPI000007ED49; EMBL:Z70718; PIDN:CAA94670.1;
A;Experimental source: clone C04G2
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C;Date: 31-Dec.1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S02388
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.2e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                              Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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us-10-712-447-210.rpr

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CygSy protein (AE006176) [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C; Species: Agrobacterium tumefaciens (c) Species: Agrobacterium tumefaciens (c) Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 (c) Accession: B98143 (c) Accession: B98144 (c) Accession: B981444 (c) Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
B.Accession: G7697
B.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ko
awa, H.; Takamiya, M.; Wasuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ko
A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caulobacter createring C;Species: Caulobacter createring C;Species: Caulobacter createring C;Accession: D87267
C;Accession: D87267
C;Accession: D87267
C;Accession: D87267
D; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Aritle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q8U6M6; UNIPARC: UPI0000D26D3; GB: AE007870; PIDN: AAK88668.1;
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Pred. No. 3.1e+02;
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33.3%; Pred. No. 2.1e+02;
tive 0; Mismatches 8;
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A;Map position: linear chromosome
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Best Local Similarity 33.3%;
Matches 4; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-710 < KUR>
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A,Status: preliminary
A,Molecule type: DNA
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A;Molecule type: DNA
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: A13144
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Accession: Al3144
A;Accession: Al3144
A;Stetus: preliminary
A;Molecule type: DNA
A;Kestdues: 1-668 *KUR.>
A;Coss-references: UNIPROT:Q846M6; UNIPARC:UPI00001649AC; GB:AE008689; PIDN:AAL45575.1;
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: linear chromosome
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C,Species: Aeropyrum pernix
C,Species: Aeropyrum pernix
C,Species: Aeropyrum pernix
C,Species: Aeropyrum pernix
C,Accession: D72453
R,Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takah DNA, Res. G, 83-101, 1999
A,Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A,Reference number: A72450; MUD:99310339; PMID:10382966
A,Accession: D72453
A,Accession: D72453
A,Accession: D72453
A,Residues: 1-660 < KAW>A,Residues: 1-660 < KAW>A,Residues: 1-660 < KAW>A,Residues: 1-660 < KAW>A,Residues: 1-600 < KAW>A,Residues: Bource: Strain Kl
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        Length 574;
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Score 18; DB 2; I
Pred. No. 2.6e+02;
0; Mismatches 8;
    Query Match
Best Local Similarity 33.3%;
Matches 4; Conservative
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Gaps

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A; Experimental source: strain H37Rv
                              C,Genetics:
A,Gene: Rv0756c
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N.Alternate names: splicing factor 9G8
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A57198; S46319
R;Popielarz, M.; Cavaloc, Y.; Mattei, M.G.; Gattoni, R.; Stevenin, J.
J. Biol. Chem. 270, 17830-17835, 1995
A;Title: The gene encoding human splicing factor 9G8. Structure, chromosomal localizatic A;Reference number: A57198, MUID:95355374; PMID:7629084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-238 <CAV>
A;Cross-references: UNIPARC:UPI0000000B853; EMBL:L22253; NID:g506401; PIDN:AAA35495.1; PI
C;Genetics:
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(970705
hypothetical protein Rv0756c - Mycobacterium tuberculosis (strain H37RV)
(5)Species: Mycobacterium tuberculosis
(5)Date: 17-010-1998 #sequence_revision 17-010-1998 #text_change 09-010-2004
(5)Accession: G70705
(6)Accession: G70705
(7)Accession: G70705
(8)Accession: G70705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:016629; UNIPARC:UPI0000000853; GB:L41887; NID:g950423; PIDN: R;Cavaloc, Y.; Popielarz, M.; Fuchs, J.P.; Gattoni, R.; Stevenin, J. B. 2639-2649; J1994
B.MBO J. 13, 2639-2649; J1994
A;Title: Characterization and cloning of the human splicing factor 9G8: a novel 35 kDa fa; Reference number: S46319; MUID:94283389; PMID:8013463
        A;Residues: 1-207 <STO>
A;Cross-references: UNIPROT:Q9ABS1; UNIPARC:UPI0000CGF4E; GB:AE005673; NID:g13421262;
C;Genetics:
A;Gene: CC0149
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                                                                                                                                          Score 17; DB 2; Length 207;
Pred. No. 2.2e+02;
0; Mismatches 8; Indels
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A;Cross-references: GDB:378350; OMIM:600572
A;Map position: 2922-292
A;Introns: 10/1; 70/2; 129/2; 154/2; 191/2; 209/2; 221/2
F;12-74/Domain: ribonucleoprotein repeat homology <RRM3>
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A;Molecule type: DNA
A;Residues: 1-238 <RES>
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A;Reference number: Z20619
A;Accession: T29423
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-310 < PAR>
A;Residues: 1-310 < PAR>
A;Cross-references: UNIPROT:O86606; UNIPARC:UPI0000DAD10; EMBL:AL031155; NID:e1313489; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein 317 - Lymantria dispar nuclear polyhedrosis virus (fragment)
N.Alternate names: ORFA protein
C.Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C.Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C.Accession: PQ0339
R.B.Biornson, R.M.; Rohrmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A.Filtle: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymant
A.Reference number: PQ0339; MUID:92300345; PMID:1607868
                                                                                                                                                                                                                                                                                                                                     C.Species: Streptomyces coelicolor
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C.Accession: T2942.
R.Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
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  Length 241;
85.0%; Score 17; DB 2; Length 241
33.3%; Pred. No. 2.6e+02;
.ive 0; Mismatches 8; Indels
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A;Molecule type: DNA
A;Residues: 1.917 < CaJO>
A;Cross-references: UNIPARC:UPI000017A7C2; DDBJ:D10836
                                                                                                                                                                                                                                                                                                           probable transposase - Streptomyces coelicolor
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Best Local Similarity 33.3
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76.532 Million cell updates/sec
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Q7RWX1_NEUCR
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
ATP-binding region, ATPase-like:Histidine kinase A, N-terminal
          Q81hv7 c
Q63x19 h
Q5y8d5 i
Q5y8d5 i
Q828d5 i
Q82y1c6 i
Q9rjr6 i
Q6eq52 c
Q6eq52 c
Q4nc22 i
Q4nc22 i
Q4lpk5 h
Q4lpk5 h
Q4lq72 g
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STRAIN=2CP-C;
US DOB Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                         DERNames-AdehDRAFT_3131;
Anaeromysobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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414 AA; 41594 MW; OADFOFODCAOBOC53 CRC64;
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AC QTRWXI NEUCR PRELIMINARY; PRT; 452 AA.

DT 01-WAR-2004 (TrEMBLrel. 26, Created)

DT 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
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Pred. No. 2.6e+02;
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EMBL; AAHD01000008; EAL79882.1; -; Genomic_DNA
ATP-binding; Kinase; Signal.
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OSW6D5 ORYSA
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Q4IQ72 GIBZE
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33.3%; P
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                                                                                                                                                                       Q4SDD4 TETNG PRELIMINARY;
Q4SDD4;
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Best Local Similarity 33...
A; Conservative
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                                                                          595 RRATSTTTRISR 606
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 4; Conservative
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                                     3 RRXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=35554;
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Matches
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                                                                                                                                                     Q4SDD4
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                                                                                                                                                                                   Adalgan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bithis T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Oui D., Ianakiev P., Redersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Roche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gherre S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Rystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Narvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., Natus O. (2020):

"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";

"The Genome Sequence shown here is derived from an EMBL/Genbank,DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                         Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Bristol N2;
MRDLINE-29060613; PubMed-2851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
BML; ACO24/94; AAK68497.1; -; Genomic DNA.
Ensembl; Y48G1BM.5; Caenorhabditis elegans.
Wormbase; WRGene00021670; Y48G1BM.5.
InterPro; IPRO08266; Tyr pkinase_AS.
InterPro; IPRO08266; Tyr pkinase_AS.
COMplete proteome; Hypothetical protein.
SEQUENCE 994 AA; I11289 MW; 73F6FC32D71D5CCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
,; AABX01000758; EAA27000.1; -; Genomic_DNA.
ENCE 452 AA; 47319 MW; F1737BB5A3111CF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein Y48G1BM.5.
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 2;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 2;
Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                994 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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33.3%; E
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33.3%; I
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Q965V1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                     Predicted protein.
Name=NCU08793.1;
                                                                                                              NCBI_TaxID=5141;
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RESULT 3

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A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Andred S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Desilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biennt C., Skalli Z., Cattolico L., Poulain J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Raris M., Volff JW., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H., Genome duplication in the teleost fish Tetraodon nigroviridis reveals T. Let early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                  Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope; Whitehead Institute Centre for Genome Research, Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry whic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 2; Length 11 Pred. No. 7.4e+02; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAB01014639; CAG01348.1; -; Genomic_DNA.
iCE 1139 AA; 121432 MW; 7E2BD59621B51FCC CRC64;
                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 3 SCAF14639, whole genome shotgun sequence.
ORFNames=GSTENG00020093001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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PRT; 1139 AA.
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SEQUENCE
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Q8DI46;
                                                                                                                                                                                                                                                      SEQUENCE
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                 Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.;
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japónica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFNames=Bcen2424DRAFT 2557;
Burkholderia cencepacia H12424.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h
Similarity 33.3%; Pred. No. 2.70+02;
4; Conservative 0; Mismatches 8: Indele
                                                                                                                                                                                             Score 19; DB 2; Length 194;
Pred. No. 2.5e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP004274; BAC83398.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Delta 1-pyrroline-5-carboxylate reductase (BC 1.5.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA; 23349 MW; E106D482D50E50C0 CRC64;
                                                                                                                                                              Complete proteome; Hypothetical protein.
SEQUENCE 194 AA; 21055 MW; D0B0D918D3F2CACB CRC64;
                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) Hypothetical protein P0450A04.111.
          PubMed=14671304; DOI=10.1126/science.1088727;
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                                                                                                                                       EMBL; AE017180; AAR34169.1; -; Genomic_DNA.
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                               95.0%;
33.3%;
                                                                                                                           Science 302:1967-1969(2003).
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Q4LNR3;
                                                                                                                                                                                     Query Match
Best Local Similarity 33.3.5
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Q7F0M2;
                                                                                                                                                                                                                                                                   139 RRSSSSLSRTTR 150
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  STRAIN=PCA / ATCC 51573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 Name=P0450A04.111;
                                                                                                                                                    GSU0839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=39947;
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                                                                                                                  environments."
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ID Q4
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DT 133
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Asa-, in which Kaa is preferably Leut, but may be other amino acids
including Pro although not Arg or Lys, and Yaa may be Pro. Amino
acid amides and methyl esters are also readily hydrolyzed, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Leucine aminopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                       STRAIN=H12424;
US DOB Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia"
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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-!- FUNCTION: Presumably involved in the processing and regular trunover of intracellular proceins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Binds 2 manganese ions per subunit (By similarity). -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -!- SIMILARITY: Belongs to the peptidase M17 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                  Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444 AA; 47128 MW; 6219556CF63899C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 2; 1 Similarity 33.3%; Pred. No. 5.9e+02; 4; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AAHL01000036; EAM17718.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
12-bable cytosol aminopeptidase (EC 3.4.11.1)
(LAP) (Leucyl aminopeptidase).
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Matches
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as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=99018118; PubMed=9799793;
Gloeckher G., Scherter S., Schattevoy R., Boright A.P., Weber J.,
Trui L.-C., Rosenthal A.;
"Large-scale sequencing of two regions in human chromosome 7q22:
analysis of 550 kb of genomic sequence around the EPO and CUTL1 loci
reveals 17 genes.";
Genome Res. 8:1060-1073 (1998).
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                                                                                                                                                                                    potential.

264 Manganese 2 (By similarity).

287 Manganese 1 and 2 (By similarity).

287 Manganese 2 (By similarity).

347 Manganese 1 (By similarity).

439 Manganese 1 and 2 (By similarity).

53090 MW, B99CBD4B015B0411 CRC64;
                                    Length 497;
                                                                                                                                                                                                                                                                       Score 19; DB 1; I
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
18-SEP-2005 (Rel. 48, Last annotation update)
PERQ amino acid rich with GYF domain protein 1.
                                                                                                                                                                                                                                                                                                                                                                                        817 AA.
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Ensembl; ENSG00000146830; Homo sapiens.
                             EMBL; BA000039; BAC09297.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reveals 17 genes.";
Senome Res. 8:1060-1073(1998).
-!- SIMILARITY: Contains 1 GYF domain.
                                                                                                                                                                            Potential
                                                                                                                                                                                                                                                                       95.0%;
33.3%;
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InterPro; IPR003169; GYF.
Pfam; PF02213; GYF; 1.
SMART; SM00444; GYF; 1.
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264 2
269 2
287 2
347 3
349 3
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nes 4; Conserv
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075420;
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METAL
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PROSITE, PS50829; GYF; 1

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Hypothetical protein.

SEQUENCE 833 AA; 87127 MW; 7P8BD43D0F4C2256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2CP-C; Use Dobe Justitute (JGI-PGF); Detter C., Glavina T., US DOE Joint Genome Institute (JGI-PGF); Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.; Anaeromyxobacter "Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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Bacteria; Protecobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
                                                                                                                                                                   Score 19; DB 1; Length 817;
Pred. No. 1.1e+03;
0; Mismatches 8; Indels
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Pred. No. 1.2e+03;
0; Mismatches 8; Indels
                                                                                                                    Poly-Gln.
C727AD2E7C2E2581 CRC64;
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Last annotation update)
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Last annotation update)
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              Poly-Glu.
Poly-Gly.
Poly-Glu.
Gln-rich.
Poly-Pro.
Poly-Glu.
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
Hypothetical protein.
ORFNames=AdehDRAFT_1669;
                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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13-SEP-2005 (TrEMBLrel. 31, La
13-SEP-2005 (TrEMBLrel. 31, La
Hypothetical protein.
ORFNames=LmjF17.1200;
                                                                                                                                      89741 MW;
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33.3%;
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33.3%;
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ID Q4QE71_LEIMA PRELIMINARY;
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Q4NSL6;
                                                                                                                                                      Query Match
Best Local Similarity 33...
Best Local 4; Conservative
                                                                                                                                                                                                                                                                             523 RRSAASSSRRSR 534
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nes 4; Conservative
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1120
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486
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STRAIN=Friedlin;
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                                                                                                  481
751
817 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania major.
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MEDLINE=96125743; PubMed=8541323; DOI=10.1016/0304-4165(95)00124-7;
Mita K., Ariyoshi N., Abe S., Takamune K., Katagiri C.;
"Structure of genes for sperm-specific nuclear basic protein (SP4) in
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Round spermatid; MEDLINE-91200205; PubMed=2015853; MEDLINE-91200205; PubMed=2015853; Milyoshi H., Uno S., Yokota T., Katagiri C., Nishida H., Takai M., Agata K., Eguchi G., Abe T.I.; Taladata K., Eguchi G., Abe T.I.; Taladation of cDNA for a Xenopus sperm-specific basic nuclear protein (SP4) and evidence for expression of SP4 mRNA in primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spermatocytes.";
Exp. Cell Res. 194:95-99 [1991).
Exp. Cell Res. 194:95-99 [1991).
-!- DEVELOPMENTAL STAGE: SP4 gene is transcribed in or before primary
-!- DEVELOPMENTAL STAGE: AP4 gene is transcribed in or before primary
spermatocyte stage but is translated at the round spermatid stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Sperm-specific nuclear basic protein (SP4).
Name-XLSP43; Synonyms-XLSP42, XLSP44;
Renopus lavvis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                  Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleosto
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus.
                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-43 AND 64-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct protein sequencing; Nuclear protein; Repeat; Sperm.
INIT MET 0 0
REPEĀT 44 51
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Biochim. Biophys. Acta 1245:430-438(1995).
EMBL; D45253; BAA08210.1; -; Genomic_DNA.
EMBL; D45253; BAA08211.1; -; Genomic_DNA.
EMBL; D45253; BAA08209.1; -; Genomic_DNA.
SEQUENCE 79 AA; 9325 MW; 920C021D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AA; 9194 MW; B342CD9CB8FD2FBA CRC64;
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Pred. No. 2e+02;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Sperm-specific basic nuclear protein SP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 AA.
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PIR; JH0404; JH0404.
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33.3%;
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Q53X49;
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                                                                                                                                  Name=SP4;
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01-FEB-2005 (TYEMBLrel. 29, Last sequence update)
01-FEB-2005 (TYEMBLrel. 29, Last sequence update)
Hyporhetical protein B1095003.55.
Name=B1095003.55;
Oryza sativa (igonica cultivar-group).
Bukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                              Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter
"Annotation of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
Submitted (UNI-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Nature 420:312-316(2002).
EMBL; AP003431; BAD82385.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 2; Length 856; 33.3%; Pred. No. 1.2e+03; ive 0; Mismatches 8; Indels
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Pred. No. 1.5e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             856 AA; 89899 MW; F33C3D7D3B663665 CRC64;
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REQUENCE 57 AA; 6587 MW; 7A9814F81F280924 CRC64;
                                                                                                                                                                                                                                                                                                                                preliminary data.
EMBL; AAHD01000021; EAL78630.1; -; Genomic_DNA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 AA
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                                                                      STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
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QSN831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           738 RRSSAAASRARR 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 33.3
Matches 4; Conservative
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                                           NUCLEOTIDE SEQUENCE
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Best Local Similarity
Matches 4; Conserv
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RESULT 13 SP4_XENLA

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RESULT 12 QSN831_ORY

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Length 78; 8; Indels

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                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Nocardiaceae, Rhodococcus.
NCBI_TaxID=1833;
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90.0%; Score 18; DB 2; Length 85;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels
Query Match

90.0%; Score 18; DB 2; Length 79;

Best Local Similarity 33.3%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
08-JUL-2004 (TrEMBLrel. 27, Last annotation update)
08-Names-BEDE.084;
Rhodococcus erythropolis.
Plasmid pBD2.
                                                                                                                                                                                                                 85 AA.
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Search completed: March 29, 2006, 01:49:13 Job time : 131.062 secs

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Sequence 11, Appl
Sequence 8, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 32376, A
Sequence 23285, A
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                                                                                                               March 29, 2006, 01:49:32 ; Search time 29.3125 Seconds (without alignments) 39.487 Million cell updates/sec
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/jaa/6_COMB.pep:*
/cgn2_6/ptodata/1/jaa/H_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
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US-09-252-991A-32376
US-09-166-930A-8
US-09-166-930A-8
US-09-905-691-4
US-09-905-691-4
US-09-905-691-5
US-09-905-691-6
US-09-905-691-7
US-09-905-691-7
US-09-252-991A-32536
US-09-252-991A-32536
US-09-252-991A-32537
US-09-252-991A-35319
US-09-252-991A-35319
US-09-252-991A-3738
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-09-252-991A-32162
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                                                                                                                                                                                                                                                                                                                                     572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext
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1 XXRRXXXXXXXX 14
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Match Length I
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Sequence 21845, Application US/09252991A
Sequence 21845, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-17
NUMBER OF SEQ ID NOS: 33142
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32376
LENGTH: 189
TYPE: PRT
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Sequence 21789, A Sequence 18191, A Sequence 14078, A P Sequence 22531, A Sequence 22531, A Sequence 17459, A Sequence 17, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 20192, A Sequence 20192, A Sequence 20193, A
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US-09-252-991A-21789
US-09-252-991A-18191
US-09-489-039A-9786
US-09-489-039A-9786
US-09-252-991A-25331
US-09-252-991A-17459
US-09-252-991A-17459
US-09-252-991A-17459
US-08-252-991A-17459
US-08-436-703B-1
US-08-436-703B-1
US-09-912-962-37
US-09-912-962-37
US-09-252-991A-20192
US-09-252-991A-20193
US-09-252-991A-20193
US-09-252-991A-20193
US-09-252-991A-20193
US-09-252-991A-20193
US-09-252-991A-2003
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1.09-252-991A-32376
1. Sequence 32376, Application US/09252991A
1. Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21845
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   Query Match
Best Local Similarity
Matches 4; Conserv
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WS-09-905-691-4

WS-09-905-691-4

Sequence 4, Application US/09905691

Patent No. 67556206

Patent No. 67556706

Patent No. 6756706

APPLICANT: Harris, Robert B.

APPLICANT: Wolz, Gabriella

APPLICANT: Wolz, Gabriella

TITLE OF INVENTION: Fluids Using Cationic Helix Peptides

TITLE OF INVENTION: Fluids Using Cationic Helix Peptides

FIRERENCE: 006338-017

CURRENT PILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 16
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US-09-166-930A-8
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Pred. No. 1.1e+02;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-166-930A-8

Sequence 8, Application US/09166930A

Sequence 8, Application US/09166930A

Patent No. 6200955

GENERAL INFORMATION:

APPLICANT: HARRIS, Robert B.

TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES

PILE REFERENCE: 006338-006

CURRENT APPLICATION NUMBER: US/09/166,930A

CURRENT FILING DATE: 1998-10-06

PRIOR PELICANTON NUMBER: US 08/660,592

PRIOR FILING DATE: 1996-06-11

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 16
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tris-Arginine Helix #3
                   TELEFAX: (703) 836-2021
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
(703) 836-6620
                                                                                                                                                                                                                                                       h
Similarity 33.3%;
4; Conservative
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                                                                                         LENGTH: 16 amino acic
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
US-08-660-592-11
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Best Local Similarity
TELEPHONE:
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Facent No. 6521795

GENERAL INFORMATION:
FALSE OF INVENTION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 442
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                                                                        Length 189;
                                                                                                                 8; Indels
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WESTERN 10. S877153

Sequence 11, Application US/08660592

PRETENT 00. S877153

GENERAL INFORMATION:

APPLICANT: SOBEL, Michael

TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSE: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STREET: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER: PEPTIDE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PATENTION DATA:

APPLICATION NUMBER: US/08/660,592

FILING DATE: 11-UTW-1996

CLASSIFICATION: Allocam X.

NAME: McGowan, Malcolm X.

NAME: McGowan, Malcolm X.

REFERENCE/DOCKET NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 006338-001

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                   Score 19; DB 2; 1
Pred. No. 4.2e+02;
0; Mismatches 8;
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                   Query Match 95.0%;
Best Local Similarity 33.3%;
Matches 4; Conservative
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Best Local Similarity
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RESULT 10
US-09-252-991A-32536
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                                                                                                                                                                                                                                                                               | Sequence 5, Application US/09905691
| Patent No. 6756206
| GENERAL INFORMATION:
| APPLICANT: Harris, Robert B.
| APPLICANT: Wolz, Russell L.
| APPLICANT: Wolz, Gabriella
| TITLE OF INVENTION: ABOORDION and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Aboorption and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Aboorption and Removal of Endotoxin from Physiological
| TITLE OF INVENTION: Abuse 1038-017
| CURRENT PAPLICATION NUMBER: US/09/905,691
| CURRENT PILING DATE: 2001-02-14
| NUMBER OF SEQ ID NOS: 5
| SEQ ID NO 5
| SEQ ID NO 5
| LENGTH: 16
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                                           Length 16;
                                                                                      8; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
CUWTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDTUM TYPE: FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIN DATA:
APPLICATION NUMBER: US/08/660,592
FLING DATE: 11-7UN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCGOWAN, MAICOLM:
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 006338-001
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Sequence 10 (Application US/08660592)
Sequence 10 (Application US/08660592)
Patent No. 1NPORMATION:
APPLICANT: HARRIS, Robert B.
APPLICANT: SCHEL, Michael
TITLE OF INVENTION: NOVEL HEARIN BINDING PEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                      90.0%; Score 18; DB 2; 1
33.3%; Pred. No. 1.1e+02;
iive 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                Best Local Similarity 33.3
Matches 4; Conservative
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US-09-905-691-5
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US-09-905-691-4
                                           Query Match
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Sequence 3235, Application US/09252991A
Sequence 3235, Application US/09252991A
Sequence 3235, Application US/09252991A
Sequence 3235, Application US/09252991A
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32536
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CURRENT APPLICATION NUMBER: US/09/905,691
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 19
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33.3%; Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
0; Mismatches 8;
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US-09-905-691-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09905691; Patent No. 6756206
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32536
TELEPHONE: (703) 836-5620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 19 aming acids
                                                                                                                                                                                                                                                    33.3%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INPORMATION:
APPLICANT: Harris, Robert B.
APPLICANT: Wolz, Russell L.
APPLICANT: Wolz, Gabriella
                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 33.5.
Best Local Similarity
4, Conservative
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Matches 4; Conservative
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                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide US-08-660-592-10
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Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-252-991A-23676
US-09-252-991A-24681
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i Sequence 2121, Application US/09252991A

i Sequence 2121, Application US/09252991A

i Sequence 2121, Application US/09252991A

i Patent No. 6551795

j GENERAL INFORMATION:

i APPLICANT: Marc J. Rubenfield et al.

i APPLICANT: Marc J. Rubenfield et al.

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

i FILE REPERBNCE: 107196.136

i CURRENT APPLICATION NUMBER: US 60/074,788

i PRIOR APPLICATION NUMBER: US 60/074,788

i PRIOR PILING DATE: 1998-02-18

i PRIOR PILING DATE: 1998-02-18

i NUMBER OF SEQ ID NOS: 33142

i SEQ ID NO 21251
                                                                                                                                                                                                                  RESULT 11
US-09-252-91A-17175
Squence 17175, Application US/09252991A
Space 1755, Application US/09252991A
Space 1715, Application US/09252991A
Space 1715, Application US/09252991A
Space 1715, Application US/09252991A
TITLE OF INVENTION: WINCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17175
LENGTH: 113
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Pred. No. 5.8e+02;
0; Mismatches 8; Indels
                    Length 103;
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                                                               8; Indels
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                    Score 18; DB 2; 1
Pred. No. 4.7e+02;
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Pred. No. 5.1e+02;
0; Mismatches 8;
                                                                 0; Mismatches
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US-09-252-991A-21251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17175
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33.3%;
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Matches 4; Conservative
                                          Best Local Similarity 33.3
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
                           Query Match
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RESULT 13

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GENERAL INFORMATION:

Factor No. 6551795

GENERAL INFORMATION:

FACTOR OF SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: MUSER: 10799-02-18

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

FRIOR PEDICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-25-991A-26906

i) Sequence 26906, Application US/09252991A

j) Patent No. 6551795

j) Patent No. 6551795

j) Patent No. 6551795

j) TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26906

LENGTH: 139

"LENGTH: 139

"TENGTH: 139
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Patent No. 655175

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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Pred. No. 6e+02;
0; Mismatches 8; Indels
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Pred. No. 6e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26906
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Similarity 33.3%;
4; Conservative
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Best Local Similarity 33.3
Matches 4; Conservative
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3, Appli 210, App 210, App 55011, 37, Appl 32306, A 147658, 350524, 1338158,

Sequence Sequence Sequence

Sequence 3 Sequence 3 Sequence 1

8, Appli 3, Appli

Sequence Seq

46297, P 72973, P 50703, P 168937, 125004,

Sequence 194527

Sequence Sequence Sequence

Run on:

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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Scene, Seeven B
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NURBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-088-198-124
; Sequence 124, Application US/10085198
; Publication No. US2004009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TILLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-279
; CURRENT APPLICATION UNBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR APPLICATION NUMBER: 60/276,401
; FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR PILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-16
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US-10-425-114-59856
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Pred. No. 2.2e+03;
                                                                                                  US-10-282-122A-50703
US-10-437-963-125004
US-10-084-846A-8
US-10-084-846A-8
US-10-084-846A-3
US-10-050-704-210
US-10-798-512-210
US-10-798-512-310
US-10-798-512-305
US-10-09-396-3306
US-10-0437-963-147658
                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-425-115-350524
US-10-425-115-338158
US-10-424-599-173763
                    US-10-437-963-150101
US-10-425-114-46297
US-10-425-114-72973
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; Sequence 59856, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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Best Local Similarity 33.3
Matches 4; Conservative
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LENGTH: 323
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Sequence 45271, A
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Sequence 104880,
Sequence 286800,
Sequence 286800,
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50352, A
48089, A
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156048,
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3948, Ap
67642, A
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                                                                                                                                                                                                        March 29, 2006, 02:05:02 ; Search time 119 Seconds
    (without alignments)
    49.156 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                                      GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd
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US-10-085-198-124
US-10-437-965-162715
US-10-084-846A-4
US-09-905-691-4
US-09-905-691-5
US-10-425-114-45271
US-10-425-115-325436
US-10-437-965-184083
US-10-437-967-184083
US-10-425-115-326800
US-10-425-115-36800
US-10-092-154-886
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US-10-425-114-4806
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US-10-437-963-156048
US-10-437-963-197400
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US-10-425-115-198672
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Maximum DB
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Result

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Gaps

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Length 323;

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Sequence 4, Application US/09905691

Sequence 4, Application US/09905691

Publication No. US20020164329A1

GENERAL INFORMATION:

APPLICANT: Harris, Robert B.

APPLICANT: Wolz, Gabriella

TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological

TITLE OF INVENTION: Aludis Using Cationic Helix Peptides

FILE REFERENCE: 006338-017

CURRENT APPLICATION NUMBER: US/09/905,691

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2. US-10-084-846A-4
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APPLICANT: Wolz, Kussell L.
APPLICANT: Wolz, Gabriella
TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
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Docal Similarity 33.3%; Pred. No. 6.1e+04;
Docal 4; Conservative 0; Mismatches 8; Indels
                              APPLICANT: MUHLENWEG, AGNES
APPLICANT: TREEZER, AXEL
TITLE OF INVENTION: ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REPRENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 4
SEC ID NO 4
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ORGANISM: Streptomyces viridochromogenes
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            APPLICANT: WEITNAUER, GABRIELE
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Sequence 162715, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zoo, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 162715

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PRIOR APPLICATION NUMBER: 60/312,858
PRIOR FILING DATE: 2001-08-16
PRIOR PELING DATE: 2001-08-16
PRIOR PELING DATE: 2001-02-27
PRIOR PLING DATE: 2001-02-27
PRIOR PLING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/286,096
PRIOR PLING DATE: 2001-04-21
PRIOR PLING DATE: 2001-04-21
PRIOR PLING DATE: 2001-06-20
PRIOR PLING DATE: 2001-06-20
PRIOR PLING DATE: 2001-08-29
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2010-02-28
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US-10-437-963-162715
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Matches 4; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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US-10-084-846A-4
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TYPE: PRT
ORGANISM: Zea mays
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Publication No. US20020164329A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Wolz, Russell L.
APPLICANT: Wolz, Gabriella
TITLE OF INVENTION: Adeorption and Removal of Endotoxin from Physiological
TITLE OF INVENTION: Pluids Using Cationic Helix Peptides
FILE REFERENCE: 006338-017
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                                                                                                                                                                                                                                  90.0%; Score 18; DB 3; Length 16; 33.3%; Pred. No. 3.5e+02; tive 0; Mismatches 8; Indels
TITLE OF INVENTION: Fluids Using Cationic Helix Peptides FILE REFERENCE: 006338-017
CURRENT PILLIQ DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 5
SEGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 16
                                                                                                                                                                                 ; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/905,691
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 19
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US-09-905-691-2
                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 4; Conserva
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US-10-437-963-184083
; Sequence 184083
; Sequence 184083 Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 184083
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; Sequence 325436, Application US/10425115
; Sequence 325436, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE REFERENCE: 38-21 (53222) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325436
; LENGTH: 118
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Pred. No. 1.4e+03;
0; Mismatches 8; Indel8
                                                                                                                                               Length 64;
                                                                                                                                               Score 18; DB 4; Length 64;
Pred. No. 1.1e+03;
0; Mismatches 8; Indels
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US-10-437-963-184083
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TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700431372_FLI.pep
US-10-425-114-45271
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Best Local Similarity 33.3%;
Matches 4; Conservative
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Best Local Similarity 33.3
Matches 4; Conservative
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Gaps

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LOCATION: (94)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (76) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                             Sequence 886 Application US/09764847

Patent No. US20020132767A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: NUMBER:

FILE REFERENCE: PC009

CURRENT APPLICANTION NUMBER: US/09/764,847

CURRENT APPLICANTION ADDATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 2003

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 886

LINGTH: 127
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                                                                                                        Score 18; DB 4; Length 124;
Pred. No. 1.9e+03;
0; Mismatches 8; Indels
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; Publication No. US20030054375A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO09C1
; CURRENT APPLICATION NUMBER: US/10/092,154
                  FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24656C.1.pep
US-10-425-115-286800
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                          Query Match 90.0%;
Best Local Similarity 33.3%;
Matches 4; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
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US-10-092-154-886
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; Sequence 286000. Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Stou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104880
LENGTH: 120
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Pred. No. 1.8e+03;
0; Mismatches 8; Indels
                                            Length 118;
                                       Score 18; DB 4; Length 118
Pred. No. 1.8e+03;
0; Mismatches 8; Indels
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US-10-437-963-104880
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LOCATION: (1)..(120)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                        Sequence 104880, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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Barbazuk, Brad
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                                            90.0%;
33.3%;
                    Query Match 90.0
Best Local Similarity 33.3
Matches 4; Conservative
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ORGANISM: Oryza sativa
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NAME/KEY: unsure
LOCATION: (1)..(124)
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ORGANISM: Zea mays
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US-10-425-115-325436
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US-10-437-963-118401

Sequence 118401, Application US/10437963

Publication No. US200401233431

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APLICATION NUMBER: US/10/437,963

CURRENT FILE REPRENCE: 38-21(53221)B

CURRENT FILE NOW SEQ ID NOS: 204966

SEQ ID NO 118401

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SEQ ID NO 118401
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                                                                                                                                                                                                                                                        LOCATION: (76)—
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATION: (88)—
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_
LOCATION: (94)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_
LOCATION: (108)
LOCATION: (108)
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VOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc. feature
LOCATION: (111)
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 1.9e+03;
0; Mismatches 8; Indels
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CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SEOFWARE: Patentin Ver. 2.0
SEOFWARE: Patentin Ver. 2.0
LENGTH: 127
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LOCATION: (1)..(134)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 33.3%;
Matches 4; Conservative
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                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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90.0%; Score 18; DB 4; Length 134;

Query Match

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Sequence 25321, A
Sequence 27148, A
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                                                                                                                                                                       March 29, 2006, 02:06:17; Search time 13.125 Seconds (without alignments) 31.461 Million cell updates/sec
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1. /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*

2. /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*

3. /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4. /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5. /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6. /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*

7. /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:*

8. /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:*
                         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-096-568A-27148

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US-11-078-469-71

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US-11-078-469-71

US-11-096-568A-20087

US-11-096-568A-10930

US-11-096-568A-1096

US-11-096-568A-22603

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US-11-096-568A-2404

US-11-096-568A-2466

US-11-096-568A-2447

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FEATURE:

Sequence Sequence Sequence

US-11-166-609-16 US-11-096-568A-25670 US-11-078-256-308

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Sequence 4518, Application US/11096568A

Sequence 4518, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: TITLE
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Squence 25321, Application US/11096568A
Squence 25321, Application US/11096568A
Squence 25321, Application No. US20060048240A1
GENERAL INFORMATION:
APPLICAMY: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592FUS2
CURRENT PAPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 25321
LEGTH: 101
TYPE: PRT
CORGANIEM: Zea mays subsp. mays
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Sequence 13882, A Sequence 7047, Ap Sequence 14539, A Sequence 22510, A Sequence 22509, A Sequence 9617, Ap Sequence 18247, A Sequence 18247, A Sequence 18247, A Sequence 18246, Ap Sequence 1855, A Sequence 18555, A Sequence 24229, A Sequence 242
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US-11-096-568A-22510
US-11-096-568A-22510
US-11-096-568A-22509
US-11-096-568A-9617
US-11-096-568A-18247
US-11-096-568A-18247
US-11-096-568A-1045
US-11-096-568A-1045
US-11-096-568A-18246
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US-11-096-568A-24216
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; LOCATION: (1)...(141)
; OTHER INFORMATION: Ceres Seq. ID no. 13638657
US-11-096-568A-4518
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Pred. No. 54;
0; Mismatches
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Best Local Similarity 33.3
Matches 4; Conservative
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                                                                                                     ORGANISM: Glycine max
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APPLICANT: HART, SCOTT A.
APPLICANT: EZH, KARIN
APPLICANT: ACHLEIDT, THOMAS
APPLICANT: STOLOW, DAVID
APPLICANT: CONGER, DES
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT PILING DATE: 2005-03-11
PRIOR PALLICATION NUMBER: 60/554,526
PRIOR PALLICATION NUMBER: 60/618,948
PRIOR PALLING DATE: 2004-01-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PALENTIN VEY: 3.3
SEQ ID NO 34
LENGTH: 32
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APPLICANT: ARRIN
APPLICANT: EEH, KARIN
APPLICANT: ACHILONG MACHLEIDT, THOMAS
APPLICANT: STOLGW, DAVID
APPLICANT: CONGER, DE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT APPLICATION NUMBER: 60/554,526
PRIOR PLILING DATE: 2004-03-18
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin Ver. 3.3
SEC ID NO 71
LENGTH: 32
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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Pred. No. 56;
0; Mismatches 8; Indels
                                                                                                             Sequence 34, Application US/11078469
Publication No. US20050282755A1
GENERAL INFORMATION:
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Publication No. US20050282755A1
GENERAL INFORMATION:
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Similarity 33.3%;
4; Conservative (
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US-11-078-469-34
  273 RRAASRSSRSRR 284
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Best Local Similarity
Matches 4; Conserva
                                                                                        US-11-078-469-34
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1592P022
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NOS: 37148
LENGTH: 341
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| Sequence 33, Application US/11182016
| Publication No. US20060019294A1
| GENERAL INFORMATION:
| APPLICANT: SUGEN, INC.
| TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
| FILE REFERENCE: 0.38602/0.102
| CURRENT APPLICATION NUMBER: US/11/182,016
| CURRENT FILING DATE: 2.005-07-15
| PRIOR APPLICATION NUMBER: US/09/958,359
| PRIOR PILING DATE: 2.002-02-05
| NUMBER OF SEQ ID NOS: 55
| SEQ ID NO 33
| SEQ ID NO 33
| LENGTH: 496
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Pred. No. 2.2e+02;
0; Mismatches 8; Indels
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                                                                                                             Score 18; DB 7; Length 101; Pred. No. 78; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
NOCATION: (1): (341)
OTHER INFORMATION: Ceres Seq. ID no. 15175533
US-11-096-568A-27148

; LOCATION: (1)...(101)
; OTHER INFORMATION: Ceres Seq. ID no. 13580080
US-11-096-568A-25321

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ORGANISM: Zea mays subsp. mays
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Best Local Similarity 33.3%;
Matches 4; Conservative
                                                                                                               Query Match
Best Local Similarity 33.3%;
Matches 4; Conservative
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ORGANISM: Unknown Organism
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NAME/KEY: misc_feature
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RESULT 9
US-11-096-568A-19930
is Sequence 19930, Application US/11096568A
publication No. US20060048240A1
GENERAL INFORMATION: Sequence Determined DNA Fragments and Corresponding Polypeptides
it TILE OF INVENTION: Therby
TILE REFERENCE: 7750-1592PUS2
CURRENT APPLICATION UNMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19930
LENGTH: 192
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Squence 16604, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REPRENCE: 2750-1592PUS.2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 16604

LENGTH: 200
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Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.0%; Score 17; DB 7; Le
33.3%; Pred. No. 2.7e+02;
iive 0; Mismatches 8;
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LOCATION: (1)...(192)
CTHER INFORMATION: Ceres Seq. ID no. 12375688
US-11-096-568A-19930
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| LOCATION: (1)...(200)
| OTHER INFORMATION: Ceres Seq. ID no. 12353107
US-11-096-5688-16604
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Best Local Similarity 33.3%;
Matches 4; Conservative
Best Local Similarity 33.3
Matches 4; Conservative
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US-11-087-099-6884
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20087
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                                                                                                                                                                                                                                                                                                                                         US-11-087-099-10728

Sequence 10728, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450) B EP

CURRENT APPLICANTION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

ENGTH: 173
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                                                                                                                                           DB 7; Length 32;
56;
                                                                                                                                                                                   8; Indels
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: LOCATION: (1)...(173)

: OTHER INFORMATION: unsure at all Xaa locations

US-11-087-099-10728
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i LOCATION: (1):(189)
cother indepartion: Ceres Seq. ID no. 12376847
US-11-096-568A-20087
                                                                                                                                                                                     0; Mismatches
                                                                                                                                             Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-096-568A-20087; Sequence 20087, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION:
    OTHER INFORMATION: peptide moiety
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                                                                                                                                           h 85.0%;
Similarity 33.3%;
4; Conservative (
                                          NAME/KEY: MOD_RES

1 LOCATION: (1)

2 OTHER INFORMATION: H2N-Arg

US-11-078-469-71
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Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
Matches 4; Conserva
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3 RRXXXXXXXX 14

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Sequence 22603, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICATOR:
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS;
CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

LENGTH: 274
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Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1952P029

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 19929
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    Score 17; DB 6; Length 274;
Pred. No. 3.5e+02;
0; Mismatches 8; Indels
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Pred. No. 3.5e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1). 7(274)
; OTHER INFORMATION: Ceres Seq. ID no. 12409336
US-11-096-568A-22603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(277)
; OTHER INFORMATION: Ceres Seq. ID no. 12375687
US-11-096-568A-19929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 29, 2006, 02:11:17 Job time : 14.125 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.0%;
  Similarity 33.3%;
4; Conservative
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                                                                                                                                 205 RRSRSASLRRSR 216
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Best Local Similarity 33.3
Matches 4; Conservative
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ORGANISM: Zea mays subsp.
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NAME/KEY: misc_feature
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Query Match
Best Local Similarity
Matches 4; Conserva
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US-11-096-568A-19929
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US-11-096-568A-20086
US-11-096-568A-20086
Sublication No. US/0060048240A1
Fublication No. US/0060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: 1592P020-2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PELICATION NUMBER: US/11/096,568A
CURRENT PELICATION NUMBER: US/11/096,568A

NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20086
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERBENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 956
LENGTH: 274
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                   Score 17; DB 7; I
Pred. No. 2.8e+02;
0; Mismatches 8;
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LOCATION: (1)...(212)

CTHER INFORMATION: Ceres Seq. ID no. 12376846

US-11-096-5688-20086
  FILE REPERENCE: 38-21(51450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 6884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-821-234-956

's Sequence 956, Application US/10821234

'publication No. US20050255114A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                     85.0%;
33.3%;
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Best Local Similarity 33.3*
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Best Local Similarity 33.3
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                              178 KRAANKAARARR 189
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CRGANISM: Homo sapiens
US-10-821-234-956
                                                                                                                                   ; TYPE: PRT
; ORGANISM: Zea mays
US-11-087-099-6884
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March 29, 2006, 01:38:52 ; Search time 159.75 Seconds
    (without alignments)
    49.507 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			071,77,7,700	
Result No.	Score	Query Match	Query Match Length DB	08	ID	Description
-	98	100.0	18	8	AD034231	Ado34231 Synthetic
2	86	100.0	18	B	AD034225	Ado34225 Synthetic
m	86	100.0	18	8	AD034228	Ado34228 Synthetic
4	86	100.0	18	8	AD034236	Ado34236 Synthetic
ĸ	86	100.0	18	æ	AD034233	Ado34233 Synthetic
v	95	96.9	18	æ	AD034314	Ado34314 Synthetic
7	94	95.9	18	œ	AD034354	
80	94	95.9	18	œ	ADO34338	Ado34338 Synthetic
0	94	95.9	18	æ	AD034352	
10	94	95.9	18	æ	ADO34340	Ado34340 Synthetic
11	94	95.9	18	æ	AD034339	Ado34339 Synthetic
12	92	93.9	18	۵	AD034297	
13	92	93.9	18	ω	AD034244	Ado34244 Synthetic
14	92	93.9	18	ω	AD034276	Ado34276 Synthetic
15	90	91.8	18	æ	AD034227	Ado34227 Synthetic
16	06	91.8	18	۵	ADO34350	Ado34350 Synthetic
17	89	90.8	18	æ	AD034322	Ado34322 Synthetic
18	88	89.8	18	Φ	ADO34336	
19	88	83.8	18	œ	AD034335	Ado34335 Synthetic
20	88	89.8	18	œ	AD034337	Ado34337 Synthetic
21	88	89.8	18	œ	ADO34241	
22	87	88.8	18	α	ADO34240	Ado34240 Synthetic
23	86	87.8	18	œ	ADO34284	Ado34284 Synthetic
24	98	87.8	18	ω	ADO34305	Ado34305 Synthetic

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AD034239 AD034344 AD034245 AD034245 AD034234 AD034343 AD0343423 AD034324 AD03428	ALIGNMENT 18 AA.	mimicking peptide,	polypeptide; rotic; cereb artery dise infarction; L; very low	œ. 1	IP. DW, Datta	E mimicking dysbetalipo equence. p; English.	novel syn further c ipoprotei cell or a comprisi ing polyn n-E mimic specific polypepti
000000000000000000000000000000000000000	de ;		ng po clerod ary a ial i	626	5821 er D	n-E 1 dy: seq: 9pp;	on on Doll not not not not
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	pepti	st entry) protein-E	mimicking F arterioscles 1; coronary myocardial protein; LDI	003WO-US03626	S-042 UND. Garb	ei se id	ates to inventi netic a combina or pla cide en lipopro libody t
0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	standard; peptide;	(fir polipo	otein-E mimi c; antiarter lesterol; cc erosis; myod ty lipoprote 		02; 2002U AB RES FO miah GM,	apolipoprot artery disea an amino ac SEQ ID NO 8;	ion rela e. The he syntl l, a re animal polypepitic apo tic apo nal ant
88 88 88 88 88 88 88 88 88 88 88 88 88		12-AUG-2004 Synthetic a	apolipoprote vasotropic; serum choles atherosclero low-density Synthetic.	7-MAY-2004 3-NOV-2003	5V-20 R-) U thara	hetic nary a rises	invent ypeptid oding t ost cel cluding icking synthe monoclo
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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL; very low density lipoprotein; VLDL.
mimicking polypeptide has the following activities: antilipaemic,
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                                                                                                                                                                                                                                                                                                               100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO34225 standard; peptide; 18 AA.
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                            Sequence 18 AA;
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cc (including animal or plant) comprising the synthetic apolipoprotein-E minicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E minicking polypeptide and a carrier; and an ennoclonal antibody that specifically binds to the synthetic apolipoprotein-E minicking polypeptide. The synthetic apolipoprotein-E minicking polypeptide has the following activities: antilipsemic, cardiant, vasotropic, antiarteriosolectoric, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is cardiant, vasotropic, antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, companies or or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (ULDL) or very low density lipoprotein (ULDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E minicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
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mimicking polypeptide encoding polynuclectide; a composition comprising
the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
an anoncolonal antibody that specifically binds to the synthetic
an monoclonal antibody that specifically binds to the synthetic
candinate a micking polypeptide. The synthetic apolipoprotein-E
mincking polypeptide has the following activities: antilipaemic,
cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
useful for reducing serum cholesterol in a subject (including a mammal
such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
chimpanzee or orangutan); for treating coronary artery disease,
dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
myocardial infarction or stroke; for breaking an embolus in the subject;
and also for treating angina. The synthetic apolipoprotein E mimicking
polypeptide enhances binding of low-density lipoprotein (LDL) or very low
density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
vibile and the subject or expressnts a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimicking polypeptide of the invention.
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Score 98; DB 8; Length 18;
Pred. No. 6.1e-08;
                       0; Indels
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  100.0%;
                                              1 GIRRFLGSIWRFIRAFYG 18
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                        18; Conservative
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ADO34236 standard; peptide; 18 AA. (first entry) 12-AUG-2004 ADO34236; RESULT 4 AD034236

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL. Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

Synthetic

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

Anantharamiah GM, Garber DW,

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. WPI; 2004-411629/38.

ö Datta

Claim 4; SEQ ID NO 13; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising

the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide at the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, comparation or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or child density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention \$

Sequence 18 AA;

Gaps ö Length 18; Indela 100.0%; Score 98; DB 8; I 100.0%; Pred. No. 6.1e-08; Mismatches ö 18; Conservative Query Match Best Local Similarity Matches 18; Conserv

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1 GIRRFLGSIWRFIRAFYG 18

> 8 ð

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Gaps ö

ADO34233 standard; peptide; 18 AA. RESULT 5 AD034233

ADO34233;

Synthetic apolipoprotein-B mimicking peptide, SEQ ID No 10. 12-AUG-2004 (first entry)

apolipoprotein-B mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina, low-density lipoprotein; LDL; very low density lipoprotein; UDL;

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

Anantharamiah GM, Garber DW, Datta

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 10; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

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an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E minicking polypeptide. The synthetic apolipoprotein-E minicking polypeptide. The synthetic apolipoprotein-E minicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is cuseful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating occonary artery disease, chimpanzee or orangutan); for treating occonary artery disease, chimpanzee or orangutan); for treating an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E minicking polypeptide of the invention.
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Sequence 18 AA;

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Gaps
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  100.0%; Score 98; DB 8; Length 18;
                        0; Indels
            Pred. No. 6.1e-08;
                         Mismatches
                         .;
0
                                                               GIRRFLGSIWRFIRAFYG 18
                                                 1 GIRRFLGSIWRFIRAFYG 18
               100.0%;
                         18; Conservative
Query Match
Best Local Similarity
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ADO34314 standard; peptide; 18 AA

(first entry) 12-AUG-2004

AD034314;

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91.

vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; mycocardial infarction; sroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;

Synthetic

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

ö Datta Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 91; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) to a cell and enhances degradation of LDL or with the acell control or the represents a synthetic apolipoprotein-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131.
                                                                                                                                                                                                                                                              Score 95; DB 8; Length 18;
Pred. No. 1.8e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                      mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO34354 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                          1 GIRRFLGSIWRFIRAFYG
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Best Local Similarity
                                                                                                                                                                                                                                     Sequence 18 AA;
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. Claim 4; SEQ ID NO 131; 79pp; English. WPI; 2004-411629/38.

Datta G;

Anantharamiah GM, Garber DW,

(UABR-) UAB RES FOUND.

13-NOV-2003; 2003WO-US036268 13-NOV-2002; 2002US-0425821P

WO2004043403-A2.

Synthetic.

27-MAY-2004

cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat. rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein-E mimicking density lipoprotein (VLDL) to a cell and enhances degradation of LDL or with by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention. mimicking polypeptide has the following activities: antilipaemic, Sequence 18 AA; 8X8888888888888X8

Gaps ö Score 94; DB 8; Length 18; Pred. No. 2.5e-07; Mismatches 0; Indels 5 1 GIRRFLGSIWRFIRAFYG 18 95.9%; Local Similarity 88.9 Query Match Matches ઠે g

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AD034338; RESULT 8 AD034338

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115. ż ADO34338 standard; peptide; 18 (first entry) 12-AUG-2004

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDDL.

Synthetic.

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

UABR-) UAB RES FOUND

ö Datta Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 115; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

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        caracter, vescetupic, autratectiverer, cereptproferer, verestipped and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, myocardial infarction or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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cerebroprotective, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
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                                                                                                                                                                                                                                                                                           95.9%; Score 94; DB 8; Length 18;
88.9%; Pred. No. 2.5e-07;
Mismatches 0; Indels
    antiarteriosclerotic,
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Best Local Similarity
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                                                                                                                                                                                                                                                                       Sequence 18 AA;
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useful for reducing serum cholesterol in a subject (including a mammal

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (ULDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                    Score 94; DB 8; Length 18;
Pred. No. 2.5e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                  Sequence 18 AA;
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              such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetaliopproteinsemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) or very low ULDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.
                                                                                                                                                                                                                                                      Score 94; DB 8; Length 18;
Pred. No. 2.5e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                          95.98;
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                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9'
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                                                                                                                                                                                                                      Sequence 18 AA;
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chimparzee or orangutan); for treating coronary artery disease, chimparzee or orangutan); for treating coronary artery disease, dysbetalioproteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
sheep, pig, human, monkey, ape,
   COW,
rat, rabbit,
   88888888888888
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888888888888

Sequence 18 AA;

Gaps . 0 Score 94; DB 8; Length 18; Pred. No. 2.5e-07; 2; Mismatches 0; Indels 1 GIRRFLGSIWRFIRAFYG 18 18 95.9**%**; 88.9**%**; 16; Conservative Local Similarity Query Match Matches g ઠે

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ADO34297 standard; peptide; 18 AA. ADO34297

(first entry)

12-AUG-2004

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina: low-density lipoprotein; LDL; very low density lipoprotein; UDDL. Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

Synthetic

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 21; 79pp; English.

Claim 4; SEQ ID NO 74; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid ancoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is mimicking polypeptide apolipoprotein-E mimicking polypeptide apolipoprotein-E mimicking polypeptide is antianginal. The synthetic apolipoprotein-E mimicking polypeptide is unseful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein. E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein. E mimicking polypeptide encoding polymelectide, a composition comprising the synthetic apolipoprotein. E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein. E mimicking polypeptide and a carrier; and an monoclonal micking polypeptide. The synthetic apolipoprotein. E mimicking polypeptide has the following activities: antilipsemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal The synthetic apolipoprotein. E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease,

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chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of mycoardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.
                                                                                                                                                                         DB 8; Length 18
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                          93.9%; Score 92; DB 8; I
88.9%; Pred. No. 5.1e-07;
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                                                                                                                                                            Query Match
Best Local Similarity 88.3.
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Local Similarity
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                                                                                                                                               Sequence 18 AA;
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for reducing serum cholesterol in a subject (including a mammal

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dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypetide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and activities: antilipaemic, cardiant, vasotropic, antiateriosofarctic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
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/note= "All Lys residues are DiMethyl-Lysine"
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                                                                                                                                                                                                 93.9%; Score 92; DB 8; I
88.9%; Pred. No. 5.1e-07;
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nes 16; Conservative
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      such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinsemia or atheroscalerosis, and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) or very low tensity lipoprotein (VDL) to a cell and enhances degradation of LDL or wimicking mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
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coronary artery disease, dysbetalipoproteinemia or atherosclerosis
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Pred. No. 5.1e-07;
2; Mismatches 0; Indels
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such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalioportotainsemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of IDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention. 88888888888888

Sequence 18 AA;

0; Gaps Query Match
91.8%; Score 90; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 29, 2006, 01:44:43 ; Search time 26.4375 Seconds (without alignments) 65.509 Million cell updates/sec

US-10-712-447-5 98 1 GIRRFLGSIWRFIRAFYG 18 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	transcription regu	2-oxoglutarate/mal	poly (3-hydroxybuty	leucyl-tRNA synthe	leucine-tRNA ligas	acriflavin resista	hypothetical prote	o	hypothetical prote	NIP1 protein - yea	TMV resistance pro	reverse transcript	penicillin-binding	c			hypothetical prote			ĕ	н	lass	HLA-A-0	class I	class I	class I hi		gene HLA-A-0205 pr
3 ID	S76462	2 A75578		2 A34341	2 A84060		2 AH3568				2 A46417						2 T15530	2 B72692	2 I54412	2 F71707	2 D97700	1 HTH069	1 HLHUA2	2 I38443	н	2 137542	2 I84448	91	2 138442
Length DB	1	178 2								516				760				237									365		
* Query Match	49.0	45.9	44.9	44.9	44.9	44.9	44.4	43.9	43.9	43.9	43.9	43.9	43.4	43.4	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	٠	•	42.9	42.9	42.9	•
Score	48	45	44	44	44	44	43.5	4	43	43	43	43	42.5		42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
Result No.	-	7	e	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote leucyl-tRNA synthe	leucyl-tRNA synthe leucyl-rRNA synthe leucine-tRNA ligas	homolog to drosoph hypothetical prote	dimethylanforde	nypothetical prote hypothetical prote probable permease		hypothetical prote cytochrome P450 DW
T04745 AD1282	AH1653 B89961 D69650	T50337 AG2115	C42595 E64109	T20575 AF2599 G97381	T08940 F96571	D96776 T02263
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30 31	332	3 3 3 4	37 38	0 4 4 0 0 1	4 4 3 2 5	4 4 5

ALIGNMENTS

RESULT 1

576462
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A; Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C,Accession: S76462
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <kan></kan>
A, Cross-references: UNIPROT: P74489; UNIPARC: UPI00000C103F; EMBL: D90915; GB: AB001339; NLD
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
Query Match 49.0%; Score 48; DB 2; Length 627;
8; Pred. No. 8.1;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

|::||||::| 597 GLEQLLGKIWQWLRQKFG 614 1 GIRRFLGSIWRFIRAFYG 18 ઠે

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A75578

Cranscription regulator, MarR family - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A5578
R;Milte, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S; Smikh, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Refatus: preliminary
A;Accession: A75578
A;Accession: A75578
A;Accession: A75578
A;Accession: A75578
A;Accession: BNA
A;Residues: 1-178 < WHI>
A;Accession: A7574
A;Accession: A7

C;Genetics: A;Gene: DRA0248 A;Map position: 2

Query Match

45.9%; Score 45; DB 2; Length 178;

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C,Accession: A84060
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Reference number: A83650, MUID:20512582; PMID:11058132
A;Accession: A84060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:09K7S8; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A;Experimental source: strain C-125
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Ruhrmann, J.L.; Geoghagen, N.S.M.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3568
                                                                                                                                                                             leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leucine-tRNA ligase (BC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-861 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
45;
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Pred. No. 48;
3; Mismatches
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.9%; Score 44;
ilarity 53.8%; Pred. No. 4
Conservative 2; Mismatch
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46.2%; Pred. No.
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100 RRFAGDAWRTNLPYRFAAAFY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: leuS
C,Superfamily: leucine-tRNA ligase
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GAKRFLGRVWNLV 677
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GARRFLDRVWRLL 634
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Best Local Similarity 46...
6; Conservative
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-806 <STO>
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                                                                                                                                                         A84060
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poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C; Special Alcaligenes eutrophus
C; Special Alcaligenes eutrophus
C; Special Alcaligenes eutrophus
C; Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C; Accession: A34341; A39190
R; Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A; Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Iden
A; Recession: A34341; MUID:89359357; PMID:2670936
A; Recession: A34341; MUID:89359357; PMID:2670936
A; Residues: preliminary
A; Molecule type: DNA
A; Status: Passon and A3434
A; Status: Passon and A3434
A; Status: Passon and A3434
A; Schubert, Passon and A3434
A; Experimental source: strain H16
B; Schubert, Passon and A3434
A; Experimental source 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiTomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, G.S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Beterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Beterson, S.; Loftus, B.; Richardson, D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Thle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64537
A;Accession: G64537
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-461 crows
A;Residues: 1-461 crows
C;Superfamily: 2-oxoglutarate/malate translocator
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A;Status: preliminary
A;Notecule type: DNA
A;Reaidues: 1-219 <SCH>
A;Reaidues: 1-219 <SCH>
A;COSS-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
C;Superfemily: poly(3-hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase
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C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
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                                           Indels
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Pred. No. 26;
2; Mismatches
                                           Mismatches
       Pred. No.
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53.8%;
   69.2%;
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   Best Local Similarity 69.2
Matches 9, Conservative
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Best Local S
Matches 10
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2 IRRFLGSIWRFIRAFYG 18
                                                                         Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 41.4.
Best Local 7; Conservative
                                                                                                                                                                                  6 LGSIWRFIRAF 16
                                                                                                                                                                                                                                   54 IGNMWSFLRAF 64
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                                                                                                                                                                                                                                                                                                                  RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F31F4.4 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C; Accession: 713216
R; Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid F31F4.
A; Reference number: 221149
A; Accession: T32316
A; Accession: T32316
A; Reference number: 221149
A; Reference number: EXILAS
A; Residues: 1-265 < BLA>
A; Residues: 1-265 < BLA>
A; Residues: 1-265 < BLA>
A; Residues: CESP: F31F4
A; Residues: CESP: F31F4
C; Genetics:
A; Genetics: A; A; Map position: 5
A; Introns: 13/3; 67/2
C; Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A,Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A,Reference number: AD3252; PMID:11756688
A,Reference HABS6B
A,Restua: Preliminary
A,Molecule type: DNA
A,Residues: 1-1025 «KUR»
A,Residues: 1-1025 «KUR»
A,Esperimental source: strain 16M
A,Experimental source: strain 16M
A,Genee: DMII0473
A,Mogene: BMII0473
A,Mogene: DMII0473
A,Mogene: More and a protein b2075
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Mterman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                        44.4%; Score 43.5; DB 2; Length 1025; 50.0%; Pred. No. 69;
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Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches
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531 FLGSVWSFMTLPRSFF 546
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                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:076442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.
A;Experimental source: strain Bristol N2; clone C2489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIPITOTO PROBLEM (Saccharomyces cerevisiae)
NyAlternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protein NyAlternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protein Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: 21-Sep-1993 #sequence-revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; SS39302
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIP1, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;MOlecule type: DNA
A;Residues: 571-582,'Q',584-640,'K',642,'K',644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:g798940; PID:g798951; MIPS:Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-110,'',112-582,'Q',584-602 <CHU>
A;Residues: 1-110,'V,'112-582,'Q',584-602 <CHU>
A;Cross-references: UNIPARC:UP10000168ACA; EMBL:Z54141; NID:g1072408; PID:g984682; MIPS
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                  ö
A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C24B9.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Reaidues: 1-812 <GUI>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849; NCBIP:117850)
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                                                                                                  Length 489
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                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D. submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C24B9
A;Reference number: Z21310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
                                                                                               Score 43; DB 2
Pred. No. 40;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.9%; Score 43; DB
41.2%; Pred. No. 42;
tive 5; Mismatches
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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: B84953
R;Shigenous, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenous, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52113
F;Cormack, R.S; Hahlbrock, K.; Somssich, I.E.
Plant J. 14, 685-92, 1998
A;Title: Isolation of putative plant transcriptional coactivators using a modified two-hymeference number: Z25848; MUID:98346011; PMID:9681033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-107 <COR>
A;Cross-references: UNIPROT:065154; UNIPARC:UPI00000C45F; EMBL:AF053302; PIDN:AAC08574.J
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: probably plays a role in gene activation during pathogen defence and planti
C; Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molccule type: DNA
A;Residues: 1-760 <STO>
A;Residues: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144
                                                                                                                                                           penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 760;
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.5; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: penicillin-binding protein 1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 29, 2006, 01:50:03 Job time : 28.4375 secs
                 178 GİRSFLGHVGFYRRFİRDF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 INRFINGKVWNFPTSIYG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 43.4%;
Local Similarity 44.4%;
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IRRFL-GSIWRFIRAFYG
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Best Local Similarity Su.v.
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: mrcB; BU200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T52113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: V
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
T04583
TWV resistance protein N homolog F23E13.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Decies: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Speciesion: 104583; T05507
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T. submitted to the Protein Sequence Database, March 1998
A;Reference number: 215378
A;Accession: T04583
A;Molecule type: DNA
A;Residues: 1-1607 <BEV>
A;Cross-references: UNIPROT: O65506; UNIPARC: UPI00000AA45C; EMBL: AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
B;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelle
A;Reference number: 215418
A;Accession: T05507
A;Accession: T05507
A;Accession: T05507
A;Accession: T469-1607 <BE2>
A;Cross-references: UNIPARC: UPI000016DBFD; EMBL: AL022373
A;Cross-references: UNIPARC: Culumbia; BAC clone T19K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reverse transcriptase homolog - fava bean (fragment)
C;Species: Vicia faba (fava bean)
C;Species: 1-6-011-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
Submitted to the EMBL Data Library, September 1997
A;Bescription: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Recession: T12085
A;Accession: T12085
A;Accession: T12085
A;Accession: T12085
A;Residues: 1-407
A;Molecule type: mRNA
A;Residues: 1-407
A;NNA
A;Residues: 1-407
A;NNA
A;Residues: 1-407
A;NNA
A;Residues: 1-407
A;NDFOT:022103; UNIPARC:UPI0000AAD3D; EMBL:AB007466; NID:d1170509;
C;Superfamily: pol polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.9%; Score 43; DB 2; Length 1607; 72.7%; Pred. No. 1.3e+02;
                                                                                                                                         Length 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.3e+02;
0; Mismatches 3; Indels
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A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270
                                                                                                                                   Score 43; DB 2;
Pred. No. 66;
4; Mismatches
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57.9%; Pred. No. 40;
tive 1; Mismatches
C;Genetics:
A;Gene: SGD:NIP1
Z;Cross-references: SGD:S0004926; MIPS:YMR309c
A;Map position: 13R
                                                                                                                                      43.9%;
53.8%;
                                                                                                                                                                                                                                                                                            |::| |{||:||:
361 GVKRILGSIFSFV 373
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                                                                                                                                            Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity
Matches 11; Conserv?
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Gaps

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1 GIRRFLGSIW---RFIRAF 16

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GenCore version 5.1.7
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M protein - p tun on:	OM protein - protein search, using sw model	March 29, 2006, 01:39:37; Search time 165.938 Seconds	76 FEBRUARY THE THE THE THE THE THE THE THE THE THE
OM protein tun on:	- pro	_	
U #	OM protein	Run on:	

Title: US-10-712-447-5 Perfect score: 98 Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Sequence: 1 GIRRFLGSIWRFIRAFYG 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

bred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		_	Q41k44 burkholderi	Q5gh72 homo sapien	Q5gh56 rattus norv		Q84zwl pisum sativ		_		6	P97035 haemophilus					Q5gh40 brachydanio	Q52e69 magnaporthe				Q5cpz7 cryptospori		-		m				_	Q4nxl6 anaeromyxob
	ΙD	Q25271 LEPDE	Q9F7V7_RHILV	Q4LK44 9BURK	Q5GH72 HUMAN	QSGH56 RAT	Q5GH64 MOUSE	Q84ZW1_PEA	Q4NQH4 9DELT	Q8R587 MOUSE	Q5GH49_FUGRU	P74489_SYNY3	P97035 HAESO	Q5U4I4_XENLA	Q52DS6 ORYSA	Q5ZPA2 9DELT	Q5GH65 MOUSE	OSGH40 BRARE	O52E69 MAGGR	XKR6 RAT	XKR6 HUMAN	SYL CHLTE	QSCPZ7 CRYPV	Q9RYR0 DEIRA	Q6L1TS_PICTO	Q7VV93 BORPE	Q7W7P3 BORPA	Q7WL31 BORBR	Q8KBA7 CHLTE	Q98D97_RHILO	Q99AQ7_9VIRU	O4NXL6 9DELT
	DB	2	7	~	7	~	7	7	~	~	~	~	~	7	N	~	~	N	~	Н	-	Н	0	~	~	~	~	~	7	7	~	N
	Length	670	735	408	579	580	580	488	188	298	578	627	240	486	910	385	540	580	618	638	641	807	2484	178	219	278	278	278	376	386	426	433
de	Query	55.1	53.1	52.0	51.0	51.0	51.0	50.0	49.0	49.0	49.0	49.0	48.5	48.0	48.0	46.9	46.9	46.9	46.9		46.9	46.9	9	45.9	45.9		45.9			45.9	45.9	45.9
	Score	54	52	51	20	50	20	4,0	48	48	48	48	47.5	47	47	46	46	46	46	46	46	46	46	45	45	45	45	45	45	45	45	45
,	Result No.	7	7	· en	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	29	30	31

08 ralstonia s m7 oryza sativ	z2 xenopus lae u8 staphylococ	fl staphylococ q8 lactobacill	98 pyrococcus	ye mus musculu 07 mus musculu	15 mus musculu	76 neurospora		v.	zl nitrosomona
Q8xg08 Q5vrm7	QScn	Q5hnf1 . Q88ug8	05jh	09cy 08bi	Q8k0	0880	M980	Q7nk	Q82t
Q8XG08_RALSO Q5VRM7_ORYSA	Q5XGZ2 XENLA SYL STAEP	SYL_STAEQ Q88008 LACPL	QSJH98_PYRKO	Q9CYY6 MOUSE	Q8K015 MOUSE	Q8X076_NEUCR	Q86WV6 HUMAN	Q7NKW3_GLOVI	Q82TZ1_NITEU
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RGO; GO: 00166821; F:ATP Binding; IEA.

RGO; GO: 0026824; F:ATP Binding; IEA.

RGO; GO: 00042626; F:ATP Base activity; IEA.

RGO; GO: 00042626; F:ATP Base activity; IEA.

RGO; GO: 0004233; F:Poptidae activity; IEA.

RGO; GO: 0006823; F:potein transport: IEA.

RGO; GO: 000855; F:potein transport: IEA.

RGO; GO: 000855; F:potein transport: IEA.

RGO; GO: 0008533; AAA ATP Base activity; IEA.

RGO; GO: 0006508; P:potein transport: IEA.

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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
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                                                                                                                                                                                                                                                               Venter A.P., Twelker S., Oresnik I.J., Hynes M.F., "Analysis of the genetic region encoding a novel rhizobiocin from Rhizobium leguminosarum bv. viciae strain 305."; Can. J. Microbiol. 47:495-502(2001).
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Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                       MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
                           Rhizobium leguminosarum (biovar viciae).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=Bcen2424DRAFT_1071;
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SWART; SM00382; AAA; I.
TIGREAMS; TIGR01846; type I sec_HlyB; 1.
PROSITE; PSS0929; ABC_TMIF; I.
PROSITE; PS00211; ABC_TRANSPORTER I; 1.
PROSITE; PSS0993; ABC_TRANSPORTER I; 1.
PROSITE; PSS0990; PEPTIDASE_C39; I.
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Q4LK44;
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Matches 10; Conservative
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
STRAIN=H12424;
US DOD Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
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                                                                                                                                                                    -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAHL01000063; EAM16412.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                            52.0%; Score 51; DB 2; Length 408; 47.1%; Pred. No. 13; ive 5; Mismatches 4; Indels
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
"A superfamily of XK-related genes (XRG) widely expressed
"A superfamily of XK-relates.";
"A superfamily of XK-relates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS34245; AAT07094.1; -; mRNA.
SEQUENCE 579 AA; 63825 MW; DBDOFF64B9EDD53D CRC64;
                                                                                                                HI2424.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.0%; Score 50; DB
ilarity 58.3%; Pred. No. 28;
Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSGH72 HUMAN PRELIMINARY;
OSGH72
10-MXY-2005 (TrEMBLrel. 30, Created)
10-MXY-2005 (TrEMBLrel. 30, Last sequin-MXY-2005 (TrEMBLrel. 30, Last sequin-MAY-2005 (TrEMBLrel. 30, Last annotation-MAY-2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 GIRQMLGHVWQWTRSSY 344
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                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 47.1
Matches 8; Conservative
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190 LGQVWRYLRALY 201
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Q5GH56;
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QRES97 MOUSE
ID QRES97 MC
AC QRES97;
DT 01-JUN-20
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                                                                                                                                                                            SEQUENCE
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Q4NQH4_9D
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963; Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.; The pea gene NA encodes ent-kaurenoic acid oxidase."; Plant Physiol. 131:335-34(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang C.-H., Chen Y.;
"A superfamily of XX-related genes (XRG) widely expressed in vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY53423; ART07102.1; -; mRNA.
MGI; MGI:3326711; AX554253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 2; Length 580;
Pred. No. 28;
3; Mismatches 2; Indels
                                                                             Score 50; DB 2; Length 580;
Pred. No. 28;
3; Mismatches 2; Indels
vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY534261; AAT07110.1; -; mRNA.
SEQUENCE 580 AA; 64337 MW; 8F4907F391B4F5BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 AA; 64301 MW; F3291FABF4C5A826 CRC64;
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-!- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; AF537321; AAO23063.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                580 AA.
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Local Similarity 58.3%;
hes 7; Conservative 3
                                                                                  58.3%;
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                                                                                                                                                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, KK-related protein 7. Name-AY534253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pisum sativum (Garden pea).
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                                                                                                                                                                                                                                                            QSGH64 MOUSE PRELIMINARY;
QSGH64;
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190 LGQVWRYLRALY 201
                                                                    Ouery Match
Best Local Similarity 58.5.
Local 7; Conservative
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190 LGQVWRYLRALY 201
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Q84ZW1;
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                                                                                                                                                 6 LGSIWRFIRAFY 17
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0842W1 PEA
1D 0842W1
DD 01-JUN
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DT 01-JUN
DE ENT-ka
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OC EUKARYV
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GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
Interpro; PER00128; Cytochrome_P450.
Interpro; IRR002401; EP4501.
Pfam; PF00067; p450; 1.
PRINTS; PR00485; BE4501.
PRINTS; PR00485; PEA501.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
Endoplasmic reticulum; Heme; Iron; Metal-binding; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=2CP-C;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
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Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
NCBI_TaxID=290397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 188;
                                                                                                                                                                                                                                                                                                                                                              Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dehalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 188 Aa; 21278 MW; 6DEAFDBF874C4721 CRC64;
                                                                                                                                                                                                                                                                                                      488 AA; 56478 MW; 503453CB6E43C830 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 49.0%; Score 48; DB 2; 1 Similarity 30.6%; Pred. No. 18; 11; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRRFLGSI-------WRFIRAFYG
                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 49; DB 58.3%; Pred. No. 34; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4NQH4 9DELT PRELIMINARY;
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Matches 7; Conservative
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54 FIGNMWSFLRAF 65
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ORFNames=AdehDRAFT 0950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
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49.0%;
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D97035_HAESO
Th P97035_HAESO PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    P74489 SYNY3 PRELIMINARY;
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185 LGQVWRYIRTMY 196
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Matches 7; Conservative
                                                                                               Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                           6 LGSIWRFIRAFY 17
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                                                                                                                                                                                                        TISSUE-Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.

Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

Expression Exp., Jordan H., Moorer L., Shenmen C.M., Schuler G.D.,

Expleton M., Soares M.B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Expleton M., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Expleton M.J., Usdin T.B., Toshiyuki S., Carninoi P., Frange C.,

Expleton M.J., Worley M.J., McKerner M.J., Abramson R.D., Mullahy S.J.,

Explain D.K., Muzwy D.M., Sodergen B.J., Lu X., Glubs R.A.,

Exhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Exhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Exhering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Explained Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Expensation and initial analysis of more than 15,000 full-length human

Expression and initial analysis of more than 15,000 full-length human
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                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Verčebrata, Euteleostomi, catinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.0%; Score 48; DB 2; Length 298; 41.2%; Pred. No. 29; 2;ve 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
XK.related protein 6.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 AA; 34043 MW; 664CE91435D9DDF8 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 578 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, BC023148; AAH23148.1; -; mRNA.
Ensembl; ENSMUSG0000020652; Mus musculus.
MGI; MGI:1923800; 2810429005Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSGH49 FUGRU PRELIMINARY;
OSGH49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sednences.
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                  2810429005Rik protein.
Name=2810429005Rik;
                                                           Mus musculus (Mouse)
                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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nes 7; Conserv
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                                                                                                                                                                                                    STRAIN=CZECH II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CZECH II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q5GH49_FUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pasteurellaceae; Histophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97221585; PubMed=9068631;
Pontarollo R.A., Rioux C.R., Potter A.A.;
"Cloning and characterization of bacteriophage-like DNA from Haemophilus somuns homologous to phages P2 and HP1.";
J. Bacteriol. 179:1872-1879(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 627;
64;
                                                                                                                                             Length 578;
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                                                                                                                                                                                                      3; Indels
vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL, BARS14268; AAT07117.1; -; mRNA.
EMBL; AYS14268; AAT07117.1; -; mRNA.
SEQUENCE 578 AA, 66214 MW; 8915B2A30D38E80D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 AA; 69724 MW; BBE187A53BF96229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. (strain PCC 6803).
Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
01f13; not preceded by a good RBS site (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                          Score 48; DB 2;
Pred. No. 58;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BA000022; BAA18591.1; -; Genomic_DNA.
PIR; S76462; S76462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xegopodinae, Xenopus, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                            Pontarollo R.A.;
Thesis (1996), V. I. D. O., University of Saskatchewan.
EMBL; U28154; AAC45167.1; -; Genomic_DNA.
NON_TER 240 240
                                                                                                                                                                                                                                                                                                                        240 240 240 MW; 63348D8619BBAC30 CRC64;
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01-FBB-2005 (TrEMBLrel. 29, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
LOC495492 protein (Fragment).
Name=LOC495492;
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              48.5%; Score 47.5; I
57.9%; Pred. No. 28;
:ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GIFQFLGGIWEHIKEAFNG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRRFLGSIWRFIR-AFYG 18
Wed Mar 29 18:01:21 2006
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4 XENLA
Q5U414_XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                     STRAIN=HS25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiative.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Length 486; Indels

48.0%; Score 47; DB 2; 50.0%; Pred. No. 70;

4; Mismatches

Best Local Similarity 50.03 Matches 9; Conservative

Query Match

174 GLREFLGSETLWPYLMAF 191 1 GIRRFLGS -- IWRFIRAF 16

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SEQUENCE 486 AA; 54035 MW; E333F97CD90A1119 CRC64;

R GO; GO:0005355; F:glucose transporter activity; IEA.
R GO; GO:000515; F:ransporter activity; IEA.
R GO; GO:000515; F:ransporter activity; IEA.
GO; GO:000515; F:ransporter activity; IEA.
GO; GO:0006215; F:ransporter activity; IEA.
R InterPro; IPR0014; MFS.
R InterPro; IPR0014; MFS.
R InterPro; IPR003629; Sub_transporter.
R InterPro; IPR00363; Sugar_transpt.
R PRIMTS; PR00172; GLUCTRNSPORT.
R PRIMTS; PR00172; GLUCTRNSPORT.
R PRIMTS; PR00172; GLUCTRNSPORT.
R PROSITE; PS50850; MFS; 1.
R PROSITE; PS50850; MFS; 1.
R PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
R Sugar_transport; Iransmembrane; Iransport.

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Gaps

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MEDLINE=2333736; Pubmed=12447438; DOI=10.1038/nature01184; MEDLINE=23337376; Pubmed=12447438; DOI=10.1038/nature01184; Asaaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Karamori H., Sa Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Adamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Adamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., An Hijshita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Arasawa W., Katagiri S., Kikuta A., Kabuchi A., Kamiya K., A karasawa W., Katagiri S., Kikuta A., Kobayashi T., Mukai Y., Nagamita K., Nakamira M., Nagashi M., Nakamima M., Nakamira M., Nakamima M., Nakamira M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Shibata M., Jamay H., Iwama H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Ano M., Jiang J., Gojobori T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Nakamo A., Nakama M., Mahan J.H., Kim H.-I., Eun M.-Y., Nakamo A., Nakama M., Jiang J., Gojobori T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Nakama M., Makama M., Jiang J., Gojobori T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Nakama M., Makama M., Makama M., Makama M., Makama M., Jiang J., Gojobori T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Makama M., Mak
                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).
Skaryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diphosphate + L-leucyl-tRNA(Leu) = AMP diphosphate + L-leucyl-tRNA(Leu).

EMBL; AP002868; BAD52586.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gramene, QSZDS6; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000482; F:Leucine-tRNA ligase activity; IEA.
GO; GO:0004829; P:Leucyl-tRNA aminoacylation; IEA.
GO; GO:0006429; P:Leucyl-tRNA aminoacylation; IEA.
                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                 910 AA.
                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002302; Leu-tRNAsyntla.
Interpro; IPR002300; tRNA-synt_la.
Interpro; IPR001412; tRNA-synt_l.
                                                                                                                                                                                                                                                       Putative leucyl-tRNA synthetase.
Name=P0698A04.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00133; tRNA-synt 1; 1
PRINTS; PR00985; TRNASYNTHLEU
                                                                 ORYSA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420:312-316(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=39947;
                                      ORYSA
                                                             QSZDS6
RESULT 14
                                                                         TISSUE-Kidney;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Bromser A.N., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Gerhard D.S.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; BC085081; AAH85081.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
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Biosynthesegenclusters aus dem Myxobakterium Angiococcus disciformis
An 48",
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ620477; CAF05655.1; -; Genomic_DNA.
InterPro; IPR001064; Crystallin.
InterPro; IPR001064; Crystallin.
PROSITE; PS550915; CRYSTALLIN BETAGAWMA; 2.
PROSITE; PS50915; CRYSTALLIN BETAGAWMA; 2.
PROSITE; PS0142; ZINC_PROTEĀSE; UNKNOWN_1.
BHYDOCHECICAL DYOCEIN.
SEQUENCE 385 AA; 43283 MW; CE609F2D64027CAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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PubMed=15324808; DOI=10.1016/j.chembiol.2004.05.014;
Sandmann A., Sasse F., Mueller R.;
"Identification and analysis of the core biosynthetic machinery of tubulysin, a potent cytotoxin with potential anticancer activity.";
Chem. Biol. 11:1071-1079(2004).
TIGRFAMS; TIGR00396; leus_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_1; 1.
ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Nucleotide-binding; Protein biosynthesis.
SEQUENCE 910 AA; 102551 MW; E58856521EC817196 CRC64;
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OSZPAZ;
OSZPAZ;
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Angiococcus disciformis.
Bacteria, Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Cystobacterineae; Cystobacterineae; Cystobacterineae; Cystobacterineae; Cystobacteria; Myxococcales; Cystobacterineae; Cy
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48.0%; Score 47; DB 2; Length 910;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels
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46.9%; Score 46; DB 2; Length 385;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 4; Mismatches 4; Indels
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March 29, 2006, 01:49:32 ; Search time 37.6875 Seconds (without alignments) 39.487 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2 6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/jaa/RE_COMB.pep:*
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	Sequence 2	Seguence 2			Sequence 24	Sequence 24						•••				Sequence 8	Sequence 8	Sequence 4	Sequence 4	Sequence 4		Sequence 4	Sequence 4			Sequence 8	Segmence 5
SUMMARIES		ID	US-08-940-095-242	US-08-940-093-242	US-08-940-096-242	US-09-465-719-242	US-09-453-605-242	US-09-453-838-242	US-08-940-136-242	US-09-453-841-242	US-09-453-833-242	US-09-453-826-242	US-09-453-840-242	US-09-865-989-242	US-09-453-834-242	US-10-283-599-242	US-09-465-718-242	US-09-205-258-892	US-10-004-860-892	US-09-586-106D-49	US-10-799-870-49	US-09-586-106D-45	US-10-799-870-45	US-08-338-882-40	US-08-338-882-41	US-09-710-279-340	US-09-134-001C-5105	US-09-328-352-8162	TIS-08-132-767-50
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Sequence 5, Appli Sequence 6620, Ap Sequence 83, Appl	Sequence 15932, A Sequence 643, App Sequence 3, Appli	Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	Sequence 1, Appli Sequence 61, Appl Sequence 1, Appli
US-08-756-317-5 US-09-134-000C-6620 US-10-360-101-83	US-09-902-540-15932 US-09-538-092-643 US-08-480-190-3	US-08-488-379-3 US-08-475-399A-3 US-08-077-255A-3	PCT-US93-07545-3 US-08-480-190-2 US-08-488-379-2	US-08-475-399A-2 US-08-077-255A-2 PCT-US93-07545-2	US-08-480-190-1 US-08-480-190-61 US-08-488-379-1
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ALIGNMENTS

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APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Guncher
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREPT: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Land COMPGILLOLE
COMPUTER: Land COMPGILLOLE
CORRENT APPLICATION DOSA
SOFTWARE: FeatSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
TILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAUKA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                 ; Sequence 242, Application US/08940095; Patent No. 6004925; GENERAL INFORMATION: APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 650-493-556
TELEX: 66141 PENUE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: No. 6004925e
US-08-940-095-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-08-940-095-242
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: N
COUNTRY:
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JS-09-465-719-242
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                                                                                                                                                                                                                                                                                 APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sexul, Renate
APPLICANT: Sexul, Renate
APPLICANT: Buttner, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Merz, Gunther
TILLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE: 258
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION.
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELEPROCOMUNICATION INFORMATION:
TELEPAX: 650-493-4935
TELEFAX: 660-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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TYPE: amino acid
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TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                         4; Mismatches
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                        Sequence 242, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 242, Application US/08940096
Patent No. 6046166
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GIRRFLGSIWRFIRAFYG 18
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                                                                                       1 GIRRFLGSIWRFIRAFYG 18
79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity 72.2 Matches 13, Conservative
                                           13; Conservative
Query Match
Best Local Similarity
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Gaps
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gequence 222. Application US/09465719
Faceta No. 6265377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Guncher
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS: 258
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKETE
COMPUTER: DISKETE
COMPUTER: DISKETE
COMPUTER: DISKETE
COMPUTER: PARTICALION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 30,742
REPLING DATE:
FILING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 2;
Pred. No. 1e-05;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIRRFLGSIWRFIRAFYG 18
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// MOLECULE TYPE: No. 6046166e

US-08-940-096-242
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Best Local Similarity 72.2%;
Matches 13; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Gaps ö

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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sexul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITT: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
REFERENCE/DOCKET NUMBER: 009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 2;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: No. 6329341e

SEQUENCE DESCRIPTION: SEQ ID NO: 242:

US-09-453-605-242
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SOFTWARE: FRAELSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION STATE
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 193-4935
TELEFAK: 650-493-556
TELEFAK: 650-493-556
TELEFAK: 65141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 18 AMINO SCIES
LENGTH: 18 AMINO SCIES
CENGTH: 18 AMINO SCIES
CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CENTRE CEN
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Patent No. 6376464
GENERAL INFORMATION:
                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                              ILEMENTE TELENTE OF TELENTE TELENTE TELENTE TELENTE SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acida TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIRRFLGSIWRFIRAFYG 18
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COM
OPERATING SYSTEM:
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; MOLECULE TYPE:
US-09-453-838-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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Patent No. 6329341
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                         APPLICATION NOTICE.
PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COCTUZAI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/OOCKET NUMBER: 600-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELERATION FON SEQ. ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO VERSION 2.0
CURRENT APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NO. 6329341-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAULA
REGISTRATION NUMBER: 30,742
                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CUPTWARE: PRESENGO Version 2.0
CUPRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GIRRFLGSIWRFIRAFYG 18
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US-09-465-719-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Bekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si:
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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US-09-453-833-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-453-841-242
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                                                                                                                                                                                                                                                                                                               APPLICANT: Sekul, Applicant Sekul, Renate APPLICANT: Buttner, Klaus APPLICANT: Cornut, Isabelle APPLICANT: Cornut, Isabelle APPLICANT: Cornut, Isabelle APPLICANT: Merz, Gunther APPLICANT: Merz, Gunther APPLICANT: Diffurcq, Jean TITLE OF INVENTION: GENE THERAPY APPROACHES TO TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-1 AGONISTS AND THEIR TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274
CORRESSED ADRESS:
ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 1036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIALD!
OURPHAIN: SYSTEM: DOS
SOFTWARE: FASTERCY VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RECISTRATION NUMBER: 30,742
TELEPHONE: 650-493-4935
TELEFONNINICATION INFORMATION:
TELEFONNINICATION INFORMATION:
TELEFONNINICATION SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                Sequence 242, Application US/08940136
Patent No. 6518412
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
                                                                                     1 GIRRFLGSIWRFIRAFYG 18
                                                                                                             1 GIRRFLGSIWRFIRAFYG 18
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    79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: No. 6518412e
US-08-940-136-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.6%;
                     Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                               US-08-940-136-242
    Query Match
                                                                                                                     g
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CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds Lip STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78; DB 2; Length 18;
Pred. No. 1e-05;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              009196-0004-999
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFENCE/DOCKET NUMBER: 009196-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 242, Application US/09453833
Patent No. 6602854
GENERAL INFORMATION:
GAPPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 amino acids
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Gaps ö

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US-00-453-840-242

US-00-453-840-242

Sequence 242, Application US/09453840

Patent No. 6716816

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Buttner, Klaus

APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: ADDIDOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    009196-0004-999
                                                                                                                009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
       PILING DATE:
PILING DATE:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,915
TELECHONE: 650-493-5556
TELEPHONE: 650-493-5556
TELERX: 66141 PENNIE
TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGIESTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 0091
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||::||||||:|| || GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: alingle
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dasseux, Jean-Louis
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Baseux, Jean-Louis
APPLICANT: Bastus
APPLICANT: Gerut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLITOR OF E-BANDERSE:
ADDRESSEE: Pennie & E-Bandel LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
COUNTRY: USA
ZIP: 10036-2811
COMPUTER: BANDALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO VETSION OF STATE.
THING DATE: US/09/453,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                          APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZAT: LAURA
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECHONNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-4935
TELEFAX: 6614 PENNIE
INFORMATION FON SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
...... amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 242, Application US/09453826
Patent No. 6630450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
           New York
                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-453-826-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                          COUNTRY:
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Cornut, Isabelle
Metz, Gunther
Mitz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1e-05; 1; Indels iive 4; Mismatches 1; Indels
                                                                                       Score 78; DB 2; Length 18;
Pred. No. 1e-05;
                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTOREY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION:
TELECHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION NUMBER: US/09/865,989

FILING DATE: 25-May-2001

CLASSIFICATION DATA:

APPLICATION NUMBER: 09/465,719

FILING DATE: 17-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: No. 6734169e SEQUENCE DESCRIPTION: SEQ ID NO: 242: US-09-865-989-242
                                                                                                                                                                                                                                                                                  Sequence 242, Application US/09865989
Patent No. 6734169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids
                                                                                                                                                            1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                  ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
                                                                                         79.6%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                           Sekul, Renate
                                                                            Query Match
Best Local Similarity 72.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 72.2
Matches 13; Conservative
STRANDEDNESS: single
                                                                                                                                                                                                                                                     SULT 12
-09-865-989-242
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JUST-09-453-814-242

Sequence 242, Application US/09453834

Sequence 242, Application US/09453834

Patent No. 6753313

GENERAL INFORMATION:
APPLICANT: Bekul, Renate
APPLICANT: Sekul, Raus
APPLICANT: Butner, Klaus
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
VENTION: GENE THERAPY APPROACHES TO
VENTION: SUPPLY APOLIPOPROTEIN A-1 AGONISTS AND THEIR
VVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION:
PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COCIUZAI, LAURA
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 6614 PERNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
"""""
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWEENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 242, Application US/10283599; Patent No. 6844327; GENERAL INFORMATION: APPLICANT: Dasseux, Jean-Louis APPLICANT: Buttner, Klaus APPLICANT: Cornut, Isabelle APPLICANT: Metz, Gunther; APPLICANT: Metz, Gunther; APPLICANT: Dufourcq, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIRRFLGSIWRFIRAFYG 18
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                      STREET: 1155 Ave
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-453-834-242
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US-10-283-599-242
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Query Match

79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels
           CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PLING DATE:
ATORNEY, AGENT INFORMATION:
NAME: COLUZZI, LAURA A
NAME: COLUZZI, LAURA A
NEGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CLARACTERSIFICS:
SEQUENCE CLARACTERSIFICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6900177e
17-Dec-1999
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GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADMRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
COUNTRY: New York
STATE: NY
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Diskette
COMPUTER: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 009196-0007-999
                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: PASTEM: DOS
SOFTWARE: PASTEM: DOS
TILING DATE: 29-CCT-2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-CCT-2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/40,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTULEA', LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-000
TELEFRONCH/ON INFORMATION:
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                                                                          SSEE: Pennie E Edmonds LLP
I: 1155 Avenue of the Americas
New York
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SOFTWARE: FRAEUSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,718
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US-09-465-718-242
Sequence 242, Application US/09465718
Patent No. 6900177
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; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
           NUMBER OF SEQUENCES: 274
                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edi
STREET: 1155 Avenue of
CITY: New York
STATE: NY
COUNTRY: USA
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Matches 18;
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LENGTH: 18
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53, Appl
74, Appl
4, Appli
127, App
99, Appl
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Sequence 5, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 13, Appl
Sequence 91, Appl
Sequence 115, Appl
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                                                                                                                                         March 29, 2006, 02:05:02 ; Search time 153 Seconds
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-13
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US-10-712-447-115
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                                                                                                                                                                                                                                                                                                                                                             1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Result

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US-10-712-447-2

| Sequence 2, Application US/10712447
| Sequence 2, Application US/10712447
| Sequence 2, Application No. US20040186057A1
| Publication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: GARBER, DAVID W. APPLICANT: GARBER, DAVID W. APPLICANT: GARBER, DAVID W. TITLE OF INVENTION: APPLICANTED OF INVENTION: APPLICANT SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING TITLE OF INVENTION: APPLICANT US/10/712,447
| TITLE OF INVENTION NUMBER: US/10/712,447
| CURRENT FILING DATE: 2003-11-13
| PRIOR FILING DATE: 2002-11-13
| NUMBER OF SEQ ID NOS: 210
| SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Sequence 5, Application US/10712447
Sequence 5, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILLE REPRENCE: 112739-12308
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT PILLING DATE: 2003-11-13
                                                                                     Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Similarity 100.0%; Pred. No. 8.8e-08;
18; Conservative 0; Mismatches 0; Indels
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APPLICANT: ANANTHARAMAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: US/03-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
SEQ ID NOS: 210
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 8
LENGTH: 18
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Sequence 10, Application US/10712447

Publication No. US20040186057A1

SEQUENCE 10. WS20040186057A1

GENERAL INFORMATION:

APPLICANT: ANDATHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: UNMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: 60/425,821

NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic potter Information: peptide US-10-712-447-8
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                                                                                                                                                                                                                                                                                         Length 18;
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100.0%; Pred. No. 8.8e-08;
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                                                                                                                                                                                                                                                                                                                                    0; Mismatches
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 5
LENGTH: 18
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                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 18; Conservative
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Matches 18; Conservative
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US-10-712-447-8
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; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
    APPLICANT: GARBER, DAVID W.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; CURRENT PILING DATE: 2003-11-13
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 91
LENGTH: 18
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Sequence 13, Application US/10712447

Publication No. US20040186057A1

Publication No. US20040186057A1

Publication No. US20040186057A1

Publication No. US20040186057A1

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

APPLICANT: APPLICANTON: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SAPOLIDOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-1234

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SEQ ID NO 13

LENGTH: 18
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Pred. No. 8.8e-08;
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100.0%; Pred. No. 8.8e-08;
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 3.2
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Matches 18; Conservative
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                       SEQ ID NO 10
LENGTH: 18
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Sequence 116, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: BANTHARAMIAH, GATTADAHALLI M.

APPLICANT: BATTA, GESTA

APPLICANT: BATTA, GESTA

TITLE OF INVENTION: APPLICAPEDENCIEIN E AND METHODS OF USE

TITLE OF INVENTION: APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER: OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                 Sequence 115, Application US/10712447

Sequence 115, Application US/10712447

Publication No. US20040186057A1

GENERAL INPORMATION:
APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIDEDROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-12308

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTIN VEY: 3.2

LENGTH: 18
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ORGANISM: Artificial Sequence
PERTUREN
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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Pred. No. 3.5e-07;
2; Mismatches 0; Indels
                                                                                                                          Query Match

96.9%; Score 95; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.5e-07;
Matches 17; Conservative 1; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Sequence 117, Application US/10712447

| Publication No. US20040186057A1
| Publication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANATHARANIAH, GATTADAHALLI M.
| APPLICANT: DATTA, GEETA
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: APPLICANT ON THE OF INVENTION: APPLICANT ON THE OF INVENTION: APPLICANT ON THE OF INVENTION: APPLICANT ON THE OF INVENTION: APPLICANT ON THE OF INVENTION: APPLICANT ON THE OF INVENTION: APPLICANT ON THE OF INVENTION: APPLICANT ON THE OFFICE OF ORTHOR OF USE
| CURRENT APPLICATION NUMBER: GO/425,821
| PRIOR FILING DATE: 2002-11-13
| NUMBER OF SEQ ID NOS: 210
| SEQ ID NO 117
| LENGTH: 18
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Sequence 129, Application US/10712447

Sequence 129, Application US/10712447

Sequence 120, Explain US/2040186057A1

GENERAL INPORMATHARAMIAH, GATTADAHALLI M.

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICATION NUMBER: US/10/712,447

CURRENT PELING DATE: 2003-11-13

PRIOR PAPLICATION NUMBER: 60/425,821

PRIOR PILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Parentin Ver. 3.2

SEQ ID NOS: 210
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
OTHER INFORMATION: peptide
US-10-712-447-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description of Artificial Sequence: Synthetic in OTHER INFORMATION: peptide US-10-712-447-117
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: peptide
US-10-712-447-116
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Best Local Similarity 88.9%; Pred. No. 3.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels
                                                                                                         Length 18
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                                                                                                            Score 94; DB 4; I Pred. No. 3.5e-07;
                                                                                                                                                                  2; Mismatches
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ORGANISM: Artificial Sequence
                                                                                                               95.9%;
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Best Local Similarity 88.99
Matches 16; Conservative
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Mismatches
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NAME/KEY: MOD RES
LOCATION: (14)
OTHER INFORMATION: (Dime) Ly8
US-10-712-447-53
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  16; Conservative
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US-10-712-447-53
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    Matches
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Sequence 131, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANATHARAMIAH, GATTADAHALLI M.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

APPLICANT: APPLICANT: SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPOTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

SOPTWARE: Patentin Ver. 3.2

SEQ ID NO 131

LENGTH: 18
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Fublication No. US20040186057A1

Fublication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMAH, GATTADAHALLI M.

APPLICANT: DATTA, GERTA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

FRIOR FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET. 3.2

SEQ ID NO 21

LENGTH: 18
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US-10-712-447-131
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US-10-712-447-21
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Pred. No. 7.1e-07;
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88.9%; Pred. No. 3.5e-07;
tive 2; Mismatches 0; Indels
                        Score 94; DB 4; Length 18;
Pred. No. 3.5e-07;
                                                                   2; Mismatches
                                                                                                                                    1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIRRFLGSIWRFIRAFYG 18
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88.9%;
                      95.9%;
88.9%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                    Query Match
Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Sequence 74, Application US/10712447

Sequence 74, Application No. US20040186057A1

Bublication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHRARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLICAPOROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT FILING DATE: 2003-11-13

PRIOR RAPLICATION NUMBER: 60/425,821

PRIOR PLING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET: 3.2

SEQ ID NOS: 210

SEC ID NO 74
Sequence 33, Application US/10712447

Sequence 33, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: AMPLICANT DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 00425,821

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET. 3.2

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide PEATURE: PARTIER: NAME/KEY: MOD_RES LOCATION: (3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; Publication No. US20040186057A1
; GENERAL INFORMATION:
APPLICANT: GARBER, DAVID W.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT APPLICATION NUMBER: 00/3-11-13
; PRIOR FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
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                                                                                                       Gaps
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Best Local Similarity 94.4%; Pred. No. 1.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                         Query Match 93.9%; Score 92; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 7.1e-07; Matches 16; Conservative 2; Mismatches 0; Indels
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                                                                                                                                          1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                       1 GIRKFLGSIWRFIKAFYG 18
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ORGANISM: Artificial Sequence
PEATURE:
; OTHER INFORMATION: peptide US-10-712-447-74
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Search completed: March 29, 2006, 02:10:39 Job time : 153 secs

1 GIRRFLGSIWRFIRAFVG 18

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March 29, 2006, 02:06:17; Search time 16.875 Seconds (without alignments) 31.461 Million cell updates/sec
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1. /SIDS5/ptodata/1/pubpaa/US06 NEW PUB.pep:*
2. /SIDS5/ptodata/1/pubpaa/US06 NEW PUB.pep:*
3. /SIDS5/ptodata/1/pubpaa/US07 NEW PUB.pep:*
4. /SIDS5/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
5. /SIDS5/ptodata/1/pubpaa/US07 NEW PUB.pep:*
6. /SIDS5/ptodata/1/pubpaa/US10 NEW PUB.pep:*
7. /SIDS5/ptodata/1/pubpaa/US10 NEW PUB.pep:*
8. /SIDS5/ptodata/1/pubpaa/US11_NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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98
1 GIRRFLGSIWRFIRAFYG 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lon		e 16672, A						198	54, 7	521				e 2589, Ap	2733,	3648,	4073,	4652,	4677,	4777,	4910,	6009	6227,		e 6911, Ap
Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
ID	US-11-096-568A-16673	US-11-096-568A-16672	US-11-096-568A-16671	US-10-793-626-340	US-09-978-360A-506	US-11-172-740-229	US-10-821-234-1575	US-10-485-517-198	US-10-392-234A-54	US-11-087-099-521	US-11-087-099-1491	US-11-087-099-1644	US-11-087-099-1700		US-11-087-099-2733	US-11-087-099-3648	US-11-087-099-4073	US-11-087-099-4652	US-11-087-099-4677	US-11-087-099-4777	US-11-087-099-4910	US-11-087-099-6008	US-11-087-099-6227	US-11-087-099-6781	US-11-087-099-6911
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% Query Match	45.9	45.9	45.9	45.9	44.9	42.9	42.9	42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8
Score	45	45	45	45	44	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
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7139, 7287, 7988, 7988, 8973, 9971, 10104, 10104, 10101, 11001, 11001, 11001, 11016, 11016, 11016, 11016, 11016, 11016, 11016, 11016, 11016, 11016, 11016,	2007
	Seguence
US-11-087-099-7139 US-11-087-099-7287 US-11-087-099-7286 US-11-087-099-7806 US-11-087-099-8837 US-11-087-099-9837 US-11-087-099-9973 US-11-087-099-10104 US-11-087-099-10104 US-11-087-099-10104 US-11-087-099-10106 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905 US-11-087-099-11905	US-11-096-568A-26625
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	514
44 44 44 44 44 44 44 44 44 44 44 44 44	41.8
	41
	45

ALIGNMENTS

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Sequence 16672, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICAT: Alexandrov, Nickolai et al. |
| APPLICAT: Alexandrov, Nickolai et al. |
| TITLE OF INVENTION: Therby |
| TITLE OF INVENTION: Therby |
| TITLE OF INVENTION: Therby |
| TITLE OF INVENTION: Therby |
| TITLE OF INVENTION: Therby |
| TITLE OF INVENTION: US/11/096,568A |
| CURRENT APPLICATION NUMBER: US/11/096,568A |
| CURRENT FILING DATE: 2005-04-01 |
| NUMBER OF SEQ ID NOS: 34471 |
| SEQ ID NO 16672 |
| LENGTH: 327
US-11-096-568A-16673
US-11-096-568A-16673, Application US/11096568A
Sequence 16673, Application NO. US20060048240A1
Publication NO. US20060048240A1
Publication NO. US20060048240A1
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1760-15929US2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 16673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 7;
Pred. No. 5.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1). (306)
| JOTHER INFORMATION: (20096-568A-16673)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| |||:|||:
200 VRESLGSLWRFM 211
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US-11-096-568A-16672
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4 RFLGSIWRFIRAFYG 18
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357 GSRRFLDRVWRLI 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-978-360A-506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SIGNAL LOCATION: -37...
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                                                                                                                                                                                                                                                                                                                                                     Sequence 16671, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-129702.
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 16671
LENGTH: 360
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NO 340
LENGTH: 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                           Score 45; DB 7; Length 327; Pred. No. 6; 2; Indels
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45.9%; Score 45; DB 6; Length 539;
Best Local Similarity 61.5%; Pred. No. 9.6;
Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 7; Length 360;
Pred. No. 6.5;
3; Mismatches 2; Indels
                      LOCATION: (1)...(327)
COTHER INFORMATION: Ceres Seq. ID no. 12353655
US-11-096-568A-16672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

: LOCATION: (1)..(360)

: OTHER INFORMATION: Ceres Seq. ID no. 12353654

US-11-096-568A-16671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.9%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                           Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                              :| |||:|||:
221 VRESLGSLWRFM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qu#cy Match
Best Local Similarity 58.3
Matches 7; Conservative
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254 VRESLGSLWRFM 265
                                                                                                                                                                                                  2 IRRFLGSIWRFI 13
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NAME/KEY: misc_feature
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Gaps

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1 GIRRFLGSIWRFI 13

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J. Sequence 229, Application US/11172740

Publication No. US20060057724A1

GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROWER, Vyacheslav
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR Norther PILLE OF INVENTION: USACHESLES IN USER IN USER IN TITLE OF INVENTION: US/11/172,740

FILE REFERENCE: 2750-1602PUS2
CURRENT APPLICATION NUMBER: US/11/172,740

PRIOR APPLICATION NUMBER: 60/583,621
                                                                                                                                                                                                                               APPLICANT: Bucklert, Aymeric
APPLICANT: Bucklert, Aymeric
APPLICANT: Bucklert, Aymeric
APPLICANT: Bucylert, Aymeric
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Complementery DNA's Encoding Proteins with Signal Peptides
TITLE OF INVENTION: Complementery DNA's Encoding Proteins with Signal Peptides
FILE REPERBNCE: 56.US4.CIP
CURRENT APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/094,121
PRIOR APPLICATION NUMBER: US 60/094,121
PRIOR FILING DATE: 1998-02-10-17
PRIOR FILING DATE: 1998-02-10-17
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR PRILING DATE: 1998-11-13
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44.9%; Score 44; DB 5; Length 379;
Best Local Similarity 53.3%; Pred. No. 9.9;
Matches 8; Conservative 2; Mismatches 5; Indels
US-09-978-360A-506
; Sequence 506, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
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sequence 54, Application US/10392234A

sequence 54, Application US/10392234A

sequence 54, Application No. US2005025538A1

GENERAL INFORMATION:
APPLICANT: Pharmacia and Upjohn Corporation
APPLICANT: Buxeer, Steven
APPLICANT: Poole, Keith
APPLICANT: Decker, Douglas
APPLICANT: Azazhi Li
APPLICANT: Azazhi Li
APPLICANT: Azazhi Li
APPLICANT: Method for Screening for acrAB Transporter Family Inhibitors
FILE REFERENCE: 6206
CURRENT APPLICATION NUMBER: US/10/392,234A
CURRENT APPLICATION NUMBER: US 60/364,935
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1

SEQ ID NO 54

LENGTH: 265
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                                                                                       Length 365;
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Pred. No. 22;
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Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFOGRATION:
GENERAL INFOGRATION:
GENERAL INFOGRATION:
GENERAL BIOSYNEXUS INCORPORATED
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
TOTIL CANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09-09
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SECTION 198
LENGTH: 805
                                                                                                                                      4; Mismatches
                                                                                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                Sequence 198, Application US/10485517; Publication No. US20050256299A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Staphylococcus aureus
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50.0%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                          42.9%;
50.0%;
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623 GSRRFLDRVWRLM 635
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ORGANISM: Escherichia coli
                                                                                                                                                                                                                 :|| |||:| ::
127 VGSDWRFLRGYH 138
                                                                                       Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575
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Best Local Similarity
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                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (13)...(81)
OTHER INFORMATION: Pfam Name: PC4; Pfam Description: Transcriptional Coactivator p15
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
OTHER INFORMATION: Utility: Useful for making lethal plants for genetic confinement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Utility: Useful for making taller plants and plants with longer; OTHER INFORMATION: inflorescences
US-11-172-740-229
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Sequence 1575, Application Wo. 102005255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR PLING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt SEQ_genes Version 1.0

SEQ ID NO 1575

LENGTH: 365
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OTHER INFORMATION: Utility: Useful for delaying flowering time
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42.9%; Score 42; DB 7; Length 85;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 8; Conservative 2; Mismatches 6; Indels
                        PRIOR APPLICATION NUMBER: 60/584,829
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 2523
SEQ ID NO 229
                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
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       FILING DATE: 2004-06-30
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NAME/KEY: misc_feature
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US-10-821-234-1575
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Indels

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NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 1644
LENGTH: 394
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Best Local Similarity
                                                                                      US-11-087-099-1644
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US-11-087-099-2589
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US-11-087-099-2733
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                                                                                                                                                   Sequence 521, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 521
LENGTH: 394
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; Publication No. US20060041961A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT PILING DATE: 2005-03-22
; SEQ ID NOS: 12464
; SEQ ID NO 1491
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
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Pred. No. 31;
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; COTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-1491
   4; Mismatches
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US-11-087-099-1644
Sequence 1644, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-521
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
 5; Conservative
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19 VGGMWAFLRAF 29
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19 VGGMWAFLRAF 29
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                                     9 IWRFIRAFYG 18
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US-11-087-099-521
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                                                                                 Score 41; DB 7; Length 394; Pred. No. 31; Mismatches 2; Indels
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Publication No. US20060041961A1
GENERAL INFORMATION: US20060041961A1
GENERAL INFORMATION: Genes and Uses for Plant Improvement;
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REPRENCE: 38-21(53450) B F9;
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 2589
LENGTH: 394
                                                                                                                                                                                                                                                                                                         Sequence 1700, Application US/11087099
Sequence 1700, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
FILLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Zea mays subsp. mays US-11-087-099-2589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Zea mays subsp. mays US-11-087-099-1700
TYPE: PRT ORGANISM: Zea mays subsp. mays
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54.5%;
                                                                                        41.8%;
                                                                                        Query Match 41.8
Best Local Similarity 54.5
Matches 6; Conservative
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Matches 6; Conservative
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19 VGGMWAFLRAF 29
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19 VGGMWAFLRAF 29
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; SEQ ID NOS: 12464; SEQ ID NO 2733; LENGTH: 394; TYPE: PRT
TYPE: PRT
CRANISM: Zea mays subsp. mays
US-11-087-099-2733
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19 VGGWWAFLRAF 29
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